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OM protein - protein search, using sw model

Run on: August 28, 2003, 19:27:31 ; Search time 52.2161 seconds
(without alignments)
902.821 Million cell updates/sec

Title: US-09-811-132-31

Perfect score: 1553
Sequence: 1 MGDHMSFLKDFLAGAVAA.....LRGNGAFVLVLEDEIRKYY 297

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1553	100.0	297 21	AAV71031 Human adenine nucl
2	1553	100.0	297 22	AAU01198 Human adenine nucl
3	1553	100.0	297 23	AAU01378 Human adenine nucl
4	1457.5	93.9	298 19	AAW61169 Ant1 protein. Mus
5	1442.5	92.9	293 22	AAU53219 Human metabolism-a
6	1398.5	90.1	298 23	AAU08516 Human insulin rece
7	1391.5	89.6	298 21	AAV71032 Human adenine nucl
8	1391.5	89.6	298 22	AAU01199 Human adenine nucl
9	1391.5	89.6	298 23	AAU01379 Human adenine nucl

10	1385.5	89.2	298 21	AAV71033
11	1385.5	89.2	298 22	AAU39641
12	1385.5	89.2	298 22	AAU01200
13	1385.5	89.2	298 23	AAU10380
14	1385.5	89.2	323 22	AAW41427
15	1294.5	83.4	325 22	ABG15423
16	1268.5	81.7	429 24	ABR41715
17	1241	79.9	299 22	ABB66082
18	1241	79.9	299 22	ABB67300
19	1221.5	78.7	263 22	ABB77056
20	1147	73.9	307 22	ABB58380
21	1101.5	70.9	315 22	ABU53218
22	1101.5	70.9	315 23	AAE21175
23	926.5	59.7	228 23	ABP43205
24	867.5	55.9	222 23	ABP74106
25	820	52.8	298 22	ABG18922
26	771	49.6	301 23	ABP73857
27	746.5	48.1	379 24	ABP81267
28	746	48.0	346 21	AAG36577
29	746	48.0	346 21	AAG37261
30	746	48.0	346 21	AAG37264
31	746	48.0	346 21	AAG38460
32	746	48.0	363 21	AAG36576
33	746	48.0	363 21	AAG37260
34	746	48.0	363 21	AAG37263
35	746	48.0	363 21	AAG38459
36	746	48.0	381 21	AAG36575
37	746	48.0	381 21	AAG37259
38	746	48.0	381 21	AAG37262
39	746	48.0	381 21	AAG38458
40	746	48.0	992 21	AAG38672
41	746	48.0	1009 21	AAG38671
42	746	48.0	1027 21	AAG38670
43	743	47.8	346 21	AAG17731
44	743	47.8	363 21	AAG17730
45	743	47.8	381 21	AAG17729

ALIGNMENTS

RESULT 1				
ID	AAV71031	standard; Protein; 297 AA.		
XX	AAV71031;			
XX	29-AUG-2000	(first entry)		
XX				
DE	Human adenine nucleotide translocator ANTL.			
DT				
XX				
XX				
KW	Human; adenine nucleotide translocator; ANTL; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; neurotrophic; antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic; antipsychotic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dytonia; diabetes; leber's hereditary optic neuropathy; schizophrenia; MLAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; myoclonic epilepsy red ragged fibre syndrome.			
KW				
KW				
XX				
OS	Homo sapiens.			
XX				
PN	WO200026370-A2.			
XX				
PD	11-MAY-2000.			
XX				
PF	03-NOV-1999;	99WO-US25883.		
XX				
XX	03-NOV-1998;	98US-0185904.		
PK	08-SEP-1999;	99US-0393441.		
XX				

PA (MITO-) MITOKOR.
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 XX
 XX WPI: 2000-365619/31.
 DR N-PSDB; AAD00519.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 PS Claim 44; Page 172; 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC d/ tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MID), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT1 from human brain.
 XX
 SQ Sequence 297 AA;
 Query Match 100.0%; Score 1553; DB 21; Length 297;
 Best Local Similarity 100.0%; Pred. No. 3.4e-173;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGDHANSFLKDFLAGAANAASVTAAPIERVKLLQOVHASKQISAERQKIIIDCVVR 60
 DB 1 MGDHANSFLKDFLAGAANAASVTAAPIERVKLLQOVHASKQISAERQKIIIDCVVR 60
 QY 61 IPKEOGFLSFWKGNLANVIRYPTQALNFAFKDKYKQLEFGVDRHKQFWRYFAGNLASG 120
 DB 61 IPKEOGFLSFWKGNLANVIRYPTQALNFAFKDKYKQLEFGVDRHKQFWRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADVGRRAQREFHGLDCTIKFKSDGLNGLYOGFNVSV 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVGRRAQREFHGLDCTIKFKSDGLNGLYOGFNVSV 180
 QY 181 OGIIIRAAVFGYDPAKAGMLPDPKRVHIFVSMIAQSVTAAGLLSYFDTYRRRMMQ 240
 DB 181 OGIIIRAAVFGYDPAKAGMLPDPKRVHIFVSMIAQSVTAAGLLSYFDTYRRRMMQ 240
 QY 241 SGRKGDIMYTGVDCKRIAKDEGAKAFKGMASNVLRGMGAFVLYLDEIKKYV 297
 DB 241 SGRKGDIMYTGVDCKRIAKDEGAKAFKGMASNVLRGMGAFVLYLDEIKKYV 297
 RESULT 2
 AAU01198
 ID AAU01198 standard; Protein; 297 AA.
 XX
 AC AAU01198;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human adenine nucleotide translocator-1 (ANT-1) protein.
 KW Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

XX OS Homo sapiens.
 XX PN WO200132876-A2.
 XX PD 10-MAY-2001.
 XX PF 03-NOV-2000; 2000WO-US30535.
 XX PR 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Frigeri LG;
 PI Velicelcib G, Davis RE;
 XX
 DR WPI: 2001-291054/30.
 DR N-PSDB; AAS05901.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 PS Disclosure; Fig 2; 186pp; English.
 XX
 CC The present sequence represents human adenine nucleotide translocator-1
 CC (ANT-1) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein.
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 XX
 SQ Sequence 297 AA;
 Query Match 100.0%; Score 1553; DB 22; Length 297;
 Best Local Similarity 100.0%; Pred. No. 3.4e-173;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGDHANSFLKDFLAGAANAASVTAAPIERVKLLQOVHASKQISAERQKIIIDCVVR 60
 DB 1 MGDHANSFLKDFLAGAANAASVTAAPIERVKLLQOVHASKQISAERQKIIIDCVVR 60
 QY 61 IPKEOGFLSFWKGNLANVIRYPTQALNFAFKDKYKQLEFGVDRHKQFWRYFAGNLASG 120
 DB 61 IPKEOGFLSFWKGNLANVIRYPTQALNFAFKDKYKQLEFGVDRHKQFWRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADVGRRAQREFHGLDCTIKFKSDGLNGLYOGFNVSV 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVGRRAQREFHGLDCTIKFKSDGLNGLYOGFNVSV 180
 QY 181 OGIIIRAAVFGYDPAKAGMLPDPKRVHIFVSMIAQSVTAAGLLSYFDTYRRRMMQ 240
 DB 181 OGIIIRAAVFGYDPAKAGMLPDPKRVHIFVSMIAQSVTAAGLLSYFDTYRRRMMQ 240
 QY 241 SGRKGDIMYTGVDCKRIAKDEGAKAFKGMASNVLRGMGAFVLYLDEIKKYV 297
 DB 241 SGRKGDIMYTGVDCKRIAKDEGAKAFKGMASNVLRGMGAFVLYLDEIKKYV 297


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QY 6 IPPEQGFSLFPMGNLANLYRPPYPTALNPAFDKTKOLELGGVDRHKOFFMFFGNLASC 120
    61 IPPEQGFSLFPMGNLANLYRPPYPTALNPAFDKTKOLELGGVDRHKOFFMFFGNLASC 120
Db 121 GAAGATSLCFVYPLDFARTLADYGR-RAQREHFGLDCLTIKTFKSDGLKGLGOGNVNS 179
    121 GAAGATSLCFVYPLDFARTLADYGRKSSQREHFGLDCLTIKTFKSDGLKGLGOGNVNS 180
QY 121 GAAGATSLCFVYPLDFARTLADYGR-RAQREHFGLDCLTIKTFKSDGLKGLGOGNVNS 179
    121 GAAGATSLCFVYPLDFARTLADYGRKSSQREHFGLDCLTIKTFKSDGLKGLGOGNVNS 180
Db 121 GAAGATSLCFVYPLDFARTLADYGRKSSQREHFGLDCLTIKTFKSDGLKGLGOGNVNS 180
    121 GAAGATSLCFVYPLDFARTLADYGRKSSQREHFGLDCLTIKTFKSDGLKGLGOGNVNS 180
QY 180 VGGIITTYRAATYGCYVDTAKGLPDPKKNHIFYSMMIAOSVTAVALGLSLSTPDTYRRRRMM 239
    181 VGGIITTYRAATYGCYVDTAKGLPDPKKNHIIYSMMIAOSVTAVALGLSLSTPDTYRRRRMM 240
Db 181 VGGIITTYRAATYGCYVDTAKGLPDPKKNHIIYSMMIAOSVTAVALGLSLSTPDTYRRRRMM 240
    181 VGGIITTYRAATYGCYVDTAKGLPDPKKNHIIYSMMIAOSVTAVALGLSLSTPDTYRRRRMM 240
QY 240 QSGRRKADIMTYGTATDCMRKIAKDGAFAFGKGAASNTLRMGGAFAVLTYLDEIKKKV 297
    241 QSGRRKADIMTYGTATDCMRKIAKDGAFAFGKGAASNTLRMGGAFAVLTYLDEIKKKV 298
Db 241 QSGRRKADIMTYGTATDCMRKIAKDGAFAFGKGAASNTLRMGGAFAVLTYLDEIKKKV 298
    241 QSGRRKADIMTYGTATDCMRKIAKDGAFAFGKGAASNTLRMGGAFAVLTYLDEIKKKV 298

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RESULT 5
AB053219
ID   AB053219 standard; Protein; 293 AA.
XX
XX
AC   AB053219;
XX
XX
DT   14-APR-2003 (first entry)
XX
XX
DE   Human metabolism-associated DKFZphes3_35n12 homologue #1.
XX
XX
KW   Human; gene therapy; vaccine; disease treatment; detection.
XX
XX
OS   Homo sapiens.
XX
XX
MO   200112659-A2.
XX
XX
PN   22-FEB-2001.
XX
XX
PE   18-AUG-2000; 2000KO-IB01496.
XX
XX
PR   18-AUG-1999; 99US-0149499.
XX
XX
PR   28-SEP-1999; 99US-0156503.
XX
XX
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
XX
XX
PI   Wleemann S;
XX
XX
DR   WPI; 2001-327840/34.
XX
XX
NC   Nucleic acids having the sequences of clones isolated from libraries of
XX
XX
XX   different human tissues, useful in recombinant DNA methodologies -
XX
XX
PS   Example III; Page 850; 1095bp; English.
XX
XX
CC   This invention describes novel polynucleotides and polypeptides isolated
CC   from human cDNA libraries which can be used for gene therapy or in
CC   vaccines. The polynucleotides of the invention and antibodies encoded by
CC   them may be used in the prevention, diagnosis and treatment of diseases
CC   associated with inappropriate polypeptide expression. The products of the
CC   invention may also be used to identify modulators of expression and
CC   activity and to down regulate expression and activity. The antibodies of
CC   the invention may also be used as diagnostic agents for detecting the
CC   presence of polypeptides in samples. This sequence represents a homologue
CC   of a polypeptide described in the disclosure of the invention.
XX
XX
SQ   Sequence 293 AA;
XX
XX
Query Match 92.9%; Score 1442.5; DB 22; Length 293;
Best Local Similarity 94.2%; Pred. No. 3e-160;
Matches 276; Conservative 10; Mismatches 6; Indels 1; Gaps 1
XX
XX
1  AMSFLKDFLAGAABAASKTAVAPLERKYLLOVQHASKOISAEKQKGIIDCVARIPE 64
1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1  ALSFLKDFLAGGIAAASKTAVAPLERKYLLOVQHASKOISAEKQKGIIDCVARIPE 60

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QY	65	QGLSEWRBNLNVIRPEPTQALNFAFDKQKOLELGGVDNKHQFMRYRFGNLSGGAAG	124
Db	61	QGLSEWRBNLNVIRPEPTQALNFAFDKTKQIFLGGVDNKHQFMRYRFGNLSGGAAG	120
QY	125	ATSLSCEVYDLDFARFRLADVGR-RAQREPHGLDCCIIRKISDGLNGLYOGFNVSVQGI	183
Db	121	ATSLSCEVYDLDFARFRLADVKGSSQREPHNLGDCILKIRKSDGLNGLYOGFNVSVQGI	180
QY	184	IYRAYAEVYDTAKGMLPDPKKNVHIIPVSMIAQSVTAAGLSTPRDTYARRRRMMQSGR	243
Db	181	IYRAYAEVYDTAKGMLPDPKKNVHI IYSMMIAQSVTAAGLSTVSPDTYARRRRMMQSGR	240
QY	244	KGADIIYGTGVCMMRIIAKDEGAKAFKFGAMSNVLRGKGAFFVYLVDLDEIKKY	296
Db	241	KGADIIYGTGTCMMRIIAKDEGAMAFKFGAMSNVLRGKGAFFVYLVDLDEIKKY	293

XX	RESULT 6
XX	AA018516
XX	AA018516 standard; Protein; 298 AA.
XX	AA018516;
XX	11-OCT-2002 (first entry)
XX	Human Insulin receptor signaling modifier SEQ ID NO: 54.
XX	Human; Insulin receptor signaling; Insulin receptor signaling modifier
XX	ISM; diabetes; metabolic syndrome; antidiabetic.
XX	Homo sapiens.
XX	WO200255664-A2.
XX	18-JUL-2002.
XX	11-JAN-2002; 2002WO-US01048.
XX	12-JAN-2001; 2001US-261226P.
XX	12-JAN-2001; 2001US-261303P.
XX	12-JAN-2001; 2001US-261304P.
XX	12-JAN-2001; 2001US-261335P.
XX	12-JAN-2001; 2001US-261336P.
XX	12-JAN-2001; 2001US-261361P.
XX	12-JAN-2001; 2001US-261456P.
XX	12-JAN-2001; 2001US-261457P.
XX	12-JAN-2001; 2001US-261458P.
XX	12-JAN-2001; 2001US-261459P.
XX	12-JAN-2001; 2001US-261461P.
XX	12-JAN-2001; 2001US-261518P.
XX	12-JAN-2001; 2001US-261531P.
XX	12-JAN-2001; 2001US-261532P.
XX	12-JAN-2001; 2001US-261589P.
XX	12-JAN-2001; 2001US-261590P.
XX	12-JAN-2001; 2001US-261694P.
XX	12-JAN-2001; 2001US-261695P.
XX	12-JAN-2001; 2001US-261697P.
XX	(EXEL-) EXELIXIS INC.
XX	Seidel-Dugan C, Ferguson KC, Kidd T;
XX	WPI; 2002-599664/64.
XX	N-PSDB; AAL48635.
XX	Identifying an Insulin receptor signaling modulator, useful as drug
XX	targets for treating diabetes or metabolic disorders, comprises
XX	contacting an assay system comprising Insulin receptor signaling
XX	modifiers with a test agent -
XX	Disclosure; Page 160-161; 232pp; English.
XX	The present invention relates to a method of identifying a candidate

insulin receptor (INR) signaling modulating agent, involving contacting an assay system comprising an insulin receptor signaling modifier (ISM) polypeptide or nucleic acid with a test agent, and detecting a test agent-biased activity of the assay system. The method is useful for identifying candidate INR signaling modulating agents. ISM genes may be used as drug targets for treatment of disorders related to INR signaling such as diabetes or metabolic syndrome. ISM nucleic acids and polypeptides are useful for identifying and testing agents that modulate ISM function and for other applications related to the involvement of ISM in INR signaling, and for identifying subjects having a predisposition to such diseases associated with INR signaling. The present sequence is an ISM protein described in the exemplification of the invention.

Sequence 298 AA;

Query Match 90.1%; Score 1398.5; DB 23; Length 298;

Best Local Similarity 88.9%; Pred. No. 4.5e-155; Mismatches 15; Indels 1; Gaps 1;

Matches 264; Conservative 17; Mismatches 15; Indels 1; Gaps 1;

1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVHASKQISAERKGIIDCYVR 60

1 MTDAAVSFAKDFLAGVAAAIKTAAPIERVKLLQVHASKQITADKQYKGIIDCYVR 60

61 IPKQGGFLSFWRGMLANVIRFPPTQALNFAFKDKYKQLFLGVDNRHKKQFWRYPAGNLASG 120

61 IPKQGGFLSFWRGMLANVIRFPPTQALNFAFKDKYKQLFLGVDNRHKKQFWRYPAGNLASG 120

121 GAAGATSLCFEYYPIDFARTRLAADYGR-AGREFHGLDCTIKIKFSKGLKYGQFNVS 179

121 GAAGATSLCFEYYPIDFARTRLAADYGR-AGREFHGLDCTIKIKFSKGLKYGQFNVS 180

180 VQGIITVRAAYGVDYFAKGMLPDPKNVHIFVSMIAQSVTAVALSTYPPDYVRRMM 239

181 VQGIITVRAAYGVDYFAKGMLPDPKNVHIFVSMIAQSVTAVALSTYPPDYVRRMM 240

240 QSGRKGADIMYTGIVDCWRKIAKDEGAKAFKGAWSNVLKMGAFVLYLDEIKKY 296

241 QSGRKGADIMYTGIVDCWRKIAKDEGAKAFKGAWSNVLKMGAFVLYLDEIKKY 297

RESULT 7

AA71032 standard; Protein: 298 AA.

AA71032; (first entry).

29-NOV-2000 (first entry).

Human adenine nucleotide translocator ANT2.

Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP; adenosine triphosphate; adenosine triphosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; neurotrophic; antiParkinsonian; cytoskeletal; antidiabetic; anticonvulsant; neuroleptic; antipsychotic; cerebroprotective; therapeutic; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MTDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.

myoclonic epilepsy red ragged fibre syndrome.

Homo sapiens.

MO200026370-A2.

11-MAY-2000.

03-NOV-1999; 99WO-US25883.

03-NOV-1998; 98US-0185904.

08-SEP-1999; 99US-0393441.

(MITO-) MITOKOR.

PA

Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR; Ghosh SS; WPT: 2000-365619/31. N-PSDB; AAD00520.

Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic agents against mitochondrial disease

Claim 45; Page 172-173; 175pp; English.

The patent discloses a method to produce adenine nucleotide translocator (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, Leber's hereditary optic neuropathy, schizophrenia, mitochondrial encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative disorders, mitochondrial diabetes and deafness (MTDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an adenine nucleotide translocator ANT2 from human brain.

Sequence 298 AA;

Query Match 89.6%; Score 1391.5; DB 21; Length 298;

Best Local Similarity 88.6%; Pred. No. 3e-154; Mismatches 16; Indels 1; Gaps 1;

Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVHASKQISAERKGIIDCYVR 60

1 MTDAAVSFAKDFLAGVAAAIKTAAPIERVKLLQVHASKQITADKQYKGIIDCYVR 60

61 IPKQGGFLSFWRGMLANVIRFPPTQALNFAFKDKYKQLFLGVDNRHKKQFWRYPAGNLASG 120

61 IPKQGGFLSFWRGMLANVIRFPPTQALNFAFKDKYKQLFLGVDNRHKKQFWRYPAGNLASG 120

121 GAAGATSLCFEYYPIDFARTRLAADYGR-AGREFHGLDCTIKIKFSKGLKYGQFNVS 179

121 GAAGATSLCFEYYPIDFARTRLAADYGR-AGREFHGLDCTIKIKFSKGLKYGQFNVS 180

180 VQGIITVRAAYGVDYFAKGMLPDPKNVHIFVSMIAQSVTAVALSTYPPDYVRRMM 239

181 VQGIITVRAAYGVDYFAKGMLPDPKNVHIFVSMIAQSVTAVALSTYPPDYVRRMM 240

240 QSGRKGADIMYTGIVDCWRKIAKDEGAKAFKGAWSNVLKMGAFVLYLDEIKKY 296

241 QSGRKGADIMYTGIVDCWRKIAKDEGAKAFKGAWSNVLKMGAFVLYLDEIKKY 297

RESULT 8

AAU01199 standard; Protein: 298 AA.

AAU01199; (first entry).

07-SEP-2001 (first entry).

Human adenine nucleotide translocator-2 (ANT-2) protein.

Human; adenine nucleotide translocator-2; ANT-2; MPT; cyclophilin; mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

Homo sapiens.

07-SEP-2001 (first entry).

Human adenine nucleotide translocator-2 (ANT-2) protein.

Human; adenine nucleotide translocator-2; ANT-2; MPT; cyclophilin; mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

OS Homo sapiens.
 PN WO200132876-A2.
 PD 10-MAY-2001.
 PE 03-NOV-2000; 2000MO-US030535.
 PR 03-NOV-1999; 9905-0434354.
 XX (MITO-) MITOKOR.
 PA Murphy AM, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
 PI Velicelceti G, Davis RE;
 DR WPI; 2001-291054/30.
 DR N-PSDB; AAS05902.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 PS
 PS Disclosure; Fig 2; 186pp; English.
 XX
 CC The present sequence represents human adenine nucleotide translocator-2
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 CC
 SQ Sequence 298 AA;
 Query Match 89.6%; Score 1391.5; DB 22; Length 298;
 Best Local Similarity 88.6%; Pred. No. 3e-154;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
 QY 1 MGDHANSFLKDFLAGAANAASVTAAVPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
 DB 1 MTDAAISFAPKDFLAGAANAASVTAAVPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKQYKQIFLGVDKRFWRYPAGNLAGS 120
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKQYKQIFLGVDKRFWRYPAGNLAGS 120
 QY 121 GAAGATSLCFVPLDFARTRLAADVGR-AOREFHGIGDCLIKIFKSDGRGLYOGFNVS 179
 DB 121 GAAGATSLCFVPLDFARTRLAADVGR-AOREFHGIGDCLIKIFKSDGRGLYOGFNVS 179
 QY 122 GAAGATSLCFVPLDFARTRLAADVGR-AOREFHGIGDCLIKIFKSDGRGLYOGFNVS 180
 DB 122 GAAGATSLCFVPLDFARTRLAADVGR-AOREFHGIGDCLIKIFKSDGRGLYOGFNVS 180
 QY 180 VGGIITIRAAVFGVYDTAKGMLPDPKNVHIFVSMIAOSVTAVAGLLSPFTVRRRMM 239
 DB 181 VGGIITIRAAVFGVYDTAKGMLPDPKNVHIFVSMIAOSVTAVAGLLSPFTVRRRMM 240
 QY 240 QSRKAGADIMYTTVCCKRIADDEGAKAFKFGANSNVLKMGGAFLVLYIDEIKKY 296
 DB 241 QSRKAGADIMYTTVCCKRIADDEGAKAFKFGANSNVLKMGGAFLVLYIDEIKKY 297

AAU10379
 ID AAU10379 standard; Protein; 298 AA.
 AC AAU10379;
 XX
 DT 14-FEB-2002 (first entry)
 DE Human adenine nucleotide translocator 2 (ANT2).
 XX Human; adenine nucleotide translocator; ANT; ss;
 KM mitochondrial matrix protein.
 XX
 OS Homo sapiens.
 PN WO200185944-A2.
 PD 15-NOV-2001.
 PE 11-MAY-2001; 2001MO-US15416.
 PR 11-MAY-2000; 2000US-0569327.
 XX
 PA (MITO-) MITOKOR.
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
 PI Ghosh SS, Moos WH, Pei Y, Carroll AK;
 DR WPI; 2002-055598/07.
 DR N-PSDB; AAS16689.
 XX
 PT Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide -
 PS
 PS Claim 44; Fig 2; 147pp; English.
 XX
 CC The invention relates to a recombinant expression construct (1)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ADP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (1) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (1) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide,
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT2.
 CC
 SQ Sequence 298 AA;
 Query Match 89.6%; Score 1391.5; DB 23; Length 298;
 Best Local Similarity 88.6%; Pred. No. 3e-154;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
 QY 1 MGDHANSFLKDFLAGAANAASVTAAVPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
 DB 1 MTDAAISFAPKDFLAGAANAASVTAAVPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKQYKQIFLGVDKRFWRYPAGNLAGS 120
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKQYKQIFLGVDKRFWRYPAGNLAGS 120
 QY 121 GAAGATSLCFVPLDFARTRLAADVGR-AOREFHGIGDCLIKIFKSDGRGLYOGFNVS 179
 DB 121 GAAGATSLCFVPLDFARTRLAADVGR-AOREFHGIGDCLIKIFKSDGRGLYOGFNVS 180
 QY 180 VGGIITIRAAVFGVYDTAKGMLPDPKNVHIFVSMIAOSVTAVAGLLSPFTVRRRMM 239

|||||
DB 181 VGGIITVRAAYFGVYDFAKGM.LPDPKNTHIVSMIAQTVAVAGLTSYPEDTVRRMM 240
OY 240 OSGRKGADIMYTGTVDCMRKTADEGAKAFKFGAMSNTLRMGAFVLYLDEIKKY 296
DB 241 OSGRKGADIMYTGTVDCMRKTADEGAKAFKFGAMSNTLRMGAFVLYLDEIKKY 297
RESULT 10
AAY71033
ID AAY71033 standard; Protein: 298 AA.
XX AAY71033;
AC
XX
XX
XX 29-AUG-2000 (first entry)
DE Human adenine nucleotide translocator ANT3.
XX
XX Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW mitochondrial permeability transition; neuroprotective; neurotropic;
KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW antiparkinsonic; cerebroprotective; therapeutic; screening; psoriasis;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
KW mitochondrial diabetes and deafness; hyperproliferative disorder;
KW myoclonic epilepsy red ragged fibre syndrome.
XX
XX Homo sapiens.
OS
XX WO200026370-A2.
PN 11-MAY-2000.
XX
XX
XX 03-NOV-1999; 99WO-US25883.
PE
XX 03-NOV-1999; 98US-0185904.
PR 08-SEP-1999; 99US-0393441.
PR
XX (MITO-) MITOKOR.
PA
XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
PI Ghosh SS;
XX
XX MPI: 2000-365619/31.
DR N-PSDB: AAD00521.
DR
XX
XX Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease -
XX
XX
XX Claim 46; Page 173-174; 175pp; English.
PS
XX
XX The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC di/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT3 from human brain.
XX
XX Sequence 298 AA;

Query Match 89.2%; Score 1385.5; DB 21; Length 298;
Best Local Similarity 87.2%; Pred No. 1.5e-153;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
OY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERYKLLQVOHASKQISARKOYKGIIDCYVR 60
DB 1 MTEQATISPAKDFLAGIAAISKTAAPVAPIERKLLQVOHASKQIAADKQKGIIDCYVR 60
OY 61 IPKEGGLSFWRGNLANVIRYPTQALNFAEDKTKQFLGVDPRHKKQFWRFAAGNLASG 120
DB 61 IPKEGGLSFWRGNLANVIRYPTQALNFAEDKTKQFLGVDPRHKKQFWRFAAGNLASG 120
OY 121 GAAGATSLCFYPLDFAPTRIAADYGR-ADREFGLDCCIIRKPSGRLGCGFVNS 179
DB 121 GAAGATSLCFYPLDFAPTRIAADYGR-ADREFGLDCCIIRKPSGRLGCGFVNS 180
OY 180 VGGIITVRAAYFGVYDFAKGM.LPDPKNTHIVSMIAQTVAVAGLTSYPEDTVRRMM 239
DB 181 VGGIITVRAAYFGVYDFAKGM.LPDPKNTHIVSMIAQTVAVAGVSYPTVRRMM 240
OY 240 OSGRKGADIMYTGTVDCMRKTADEGAKAFKFGAMSNTLRMGAFVLYLDEIKKY 297
DB 241 OSGRKGADIMYTGTVDCMRKTADEGAKAFKFGAMSNTLRMGAFVLYLDEIKKY 298
RESULT 11
AAM39641
ID AAM39641 standard; Protein: 298 AA.
XX
XX AAM39641;
AC
XX
XX 22-OCT-2001 (first entry)
DE
XX
XX Human polypeptide SEQ ID NO 2786.
DE
XX
XX Human; neurotropic; immunosuppressant; cytosolic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
XX Homo sapiens.
OS
XX WO200153312-A1.
PN
XX
XX 26-JUL-2001.
PD
XX
XX 26-DEC-2000; 2000WO-US34263.
PE
XX
XX 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0692036.
PR 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
PA
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao Q, Zhou P, Goodrich R, Drmanac RT;
XX
XX MPI: 2001-442253/47.
DR N-PSDB: AAI58797.
DR
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
PT
XX
XX Example 4; SEQ ID NO 2786; 10078pp; English.
PS

XX The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AA438642-AA442213) with neurotrophic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX
 SQ Sequence 298 AA;
 Query Match 89.2%; Score 1385.5; DB 22; Length 298;
 Best Local Similarity 87.2%; Pred. No. 1.5e-153;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
 OY 1 MGDHMSFLDLAGAFAAASKTAVAPIERVKLLQVQASHQISAEKQYKGIIDCVR 60
 DB 1 MTEQALSFARDFLAGGIAAISKTAAPIRVRKLLQVQASHQIADKQYKGIIDCVR 60
 OY 61 IPKEGFLSWRGNLANVIRYFPQALNFAFKDKYKOLFSGVDNRHQRFRYFAGNLSG 120
 DB 61 IPKEGFLSWRGNLANVIRYFPQALNFAFKDKYKOLFSGVDNRHQRFRYFAGNLSG 120
 OY 121 GAAGATSLCFVYPLDFARTRIADVGR- AOREPHGLGDCITIKFSDGLRGLYOGFNVS 179
 DB 121 GAAGATSLCFVYPLDFARTRIADVGR- AOREPHGLGDCITIKFSDGLRGLYOGFNVS 180
 OY 180 VOGIIIRAAVFGYDTAKGMLPDPKRVHLFVSMIMQSTAVAGLSYFPDVRRRMM 239
 DB 181 VOGIIIRAAVFGYDTAKGMLPDPKRVHLFVSMIMQSTAVAGLSYFPDVRRRMM 240
 OY 240 QSGRKADIMYTGTVDCWRKIADDEGAKAFKAGMSVNLGKMGAFVLYIDEIKKYV 297
 DB 241 QSGRKADIMYTGTVDCWRKIADDEGAKAFKAGMSVNLGKMGAFVLYIDEIKKYV 298
 RESULT 12
 AAU01200 standard; Protein: 298 AA.
 ID AAU01200;
 AC AAU01200;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human adenine nucleotide translocator-3 (ANT-3) protein.
 XX
 KW Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;
 KW mitochondrial permeability translocator pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200132876-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-US30535.
 XX
 PR 03-NOV-1999; 99US-0434354.
 XX
 XX (MITO-) MITOKOR.
 PA
 XX
 PI Murphy AN, Clevenger W, Willey SE, Andreyev AY, Frigieri LG;

PI Velicelebi G, Davis RE;
 XX
 DR WPI: 2001-291054/30.
 DR N-PSDB: AAS05903.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability translocator (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 PS Disclosure; Fig 2; 186pp; English.
 XX
 CC The present sequence represents human adenine nucleotide translocator-3
 CC (ANT-3) protein. ANT proteins are mitochondrial permeability
 CC translocator (MTP) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 XX
 SQ Sequence 298 AA;
 Query Match 89.2%; Score 1385.5; DB 22; Length 298;
 Best Local Similarity 87.2%; Pred. No. 1.5e-153;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
 OY 1 MGDHMSFLDLAGAFAAASKTAVAPIERVKLLQVQASHQISAEKQYKGIIDCVR 60
 DB 1 MTEQALSFARDFLAGGIAAISKTAAPIRVRKLLQVQASHQIADKQYKGIIDCVR 60
 OY 61 IPKEGFLSWRGNLANVIRYFPQALNFAFKDKYKOLFSGVDNRHQRFRYFAGNLSG 120
 DB 61 IPKEGFLSWRGNLANVIRYFPQALNFAFKDKYKOLFSGVDNRHQRFRYFAGNLSG 120
 OY 121 GAAGATSLCFVYPLDFARTRIADVGR- AOREPHGLGDCITIKFSDGLRGLYOGFNVS 179
 DB 121 GAAGATSLCFVYPLDFARTRIADVGR- AOREPHGLGDCITIKFSDGLRGLYOGFNVS 180
 OY 180 VOGIIIRAAVFGYDTAKGMLPDPKRVHLFVSMIMQSTAVAGLSYFPDVRRRMM 239
 DB 181 VOGIIIRAAVFGYDTAKGMLPDPKRVHLFVSMIMQSTAVAGLSYFPDVRRRMM 240
 OY 240 QSGRKADIMYTGTVDCWRKIADDEGAKAFKAGMSVNLGKMGAFVLYIDEIKKYV 297
 DB 241 QSGRKADIMYTGTVDCWRKIADDEGAKAFKAGMSVNLGKMGAFVLYIDEIKKYV 298
 RESULT 13
 AAU10380 standard; Protein: 298 AA.
 ID AAU10380;
 AC AAU10380;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human adenine nucleotide translocator 3 (ANT3).
 XX
 KW Human; adenine nucleotide translocator; ANT3;
 KW mitochondrial matrix protein.
 XX
 OS Homo sapiens.

```

XX  WO200185944-A2.
XX  15-NOV-2001.
XX  11-MAY-2001; 2001WO-US15416.
XX  11-MAY-2000; 2000US-0569327.
XX  (MITO-) MITOKOR.
XX  Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
PI  Ghosh SS, Moos WH, Pei Y, Carroll AK;
XX  WPI: 2002-055598/07.
XX  N-PSDB: AAS16690.
XX  Novel recombinant expression construct for producing adenine nucleotide
PT  translocator polypeptides, comprises a regulated promoter linked to
PT  nucleic acid encoding the polypeptide
XX  Example 3; Fig 2; 147pp; English.
XX  The invention relates to a recombinant expression construct (I)
CC  comprising a regulated promoter operably linked to a nucleic acid
CC  encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
CC  proteins mediate the exchange of ATP synthesised in the mitochondrial
CC  matrix for ADP in the cytosol. (I) is useful for producing recombinant
CC  ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
CC  culturing the host cell. (I) is also useful for targeting a polypeptide
CC  of interest to a mitochondrial membrane, where ANT polypeptide is
CC  expressed as a fusion protein with the polypeptide of interest.
CC  Recombinant ANT polypeptide, or cells expressing the polypeptide, is
CC  useful for identifying an agent that binds to an ANT polypeptide. ANT
CC  ligand is useful for determining the presence of an ANT polypeptide,
CC  preferably ANTF1, ANTF2 or ANTF3 in a biological sample and for isolating
CC  ANT from a biological sample, where the ANT ligand is covalently or non-
CC  covalently bound to a solid phase. Detectably labeled ANT ligand is also
CC  useful for identifying an agent that interacts with an ANT polypeptide.
CC  The present sequence represents the amino acid sequence of human ANTF3.
XX  SO  Sequence 298 AA;
XX  Query Match 89.2%; Score 1385.5; DB 23; Length 298;
XX  Best Local Similarity 87.2%; Pred. No. 1.5e-153;
XX  Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
XX  QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHSKQISAEKQKGIIDCYVR 60
XX  I : I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
XX  1 MTEQAISFAKDFLAGGIAAASKTAVAPIERVKLLQVQHSKQIAADKQKGYIDCYVR 60
XX  DB 61 IPKEGGLSFWRGNLANVIRFPPTQALNFAFKDKYKQFLGVDNKHQFMRFFAGNLSG 120
XX  I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
XX  61 IPKEGGLSFWRGNLANVIRFPPTQALNFAFKDKYKQFLGVDNKHQFMRFFAGNLSG 120
XX  DB 121 GAAGATSCIFYPLDFAFTRILADVGR- AQRFFHGLDCTIIKFKSDGLNGLYGFQFVNS 179
XX  I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
XX  121 GAAGATSCIFYPLDFAFTRILADVGR- AQRFFHGLDCTIIKFKSDGLNGLYGFQFVNS 179
XX  QY 121 GAAGATSCIFYPLDFAFTRILADVGR- AQRFFHGLDCTIIKFKSDGLNGLYGFQFVNS 179
XX  I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
XX  121 GAAGATSCIFYPLDFAFTRILADVGR- AQRFFHGLDCTIIKFKSDGLNGLYGFQFVNS 180
XX  DB 121 GAAGATSCIFYPLDFAFTRILADVGR- AQRFFHGLDCTIIKFKSDGLNGLYGFQFVNS 180
XX  I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
XX  121 GAAGATSCIFYPLDFAFTRILADVGR- AQRFFHGLDCTIIKFKSDGLNGLYGFQFVNS 180
XX  QY 180 VQGIIITRAAFYGYDTAKGMLPDPKKNHIEVSMIAQSVAVAGLSYFEDTVARRMM 239
XX  I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
XX  180 VQGIIITRAAFYGYDTAKGMLPDPKKNHIEVSMIAQSVAVAGLSYFEDTVARRMM 239
XX  DB 181 VQGIIITRAAFYGYDTAKGMLPDPKKNHIEVSMIAQSVAVAGLSYFEDTVARRMM 240
XX  I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
XX  181 VQGIIITRAAFYGYDTAKGMLPDPKKNHIEVSMIAQSVAVAGLSYFEDTVARRMM 240
XX  QY 240 QSGRGADIMYTGVDCAWKRIAKDEGAFAFFGANSVNLRGGAFFVVLDEIRKKY 297
XX  I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
XX  240 QSGRGADIMYTGVDCAWKRIAKDEGAFAFFGANSVNLRGGAFFVVLDEIRKKY 297
XX  DB 241 QSGRGADIMYTGVDCAWKRIAKDEGAFAFFGANSVNLRGGAFFVVLDEIRKKY 298
XX  I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
XX  241 QSGRGADIMYTGVDCAWKRIAKDEGAFAFFGANSVNLRGGAFFVVLDEIRKKY 298
XX  RESULT 14
XX  ID AAM41427 standard; Protein: 323 AA.
XX  AC AAM41427;

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XX  22-OCT-2001 (first entry)
XX  Human polypeptide SEQ ID NO 6358.
XX  DE Human polypeptide SEQ ID NO 6358.
XX  KW Human; nocotropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX  KW peripheral nervous system; neuropathy; central nervous system; CNS;
XX  KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX  KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX  KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
XX  KW leukaemia.
XX  OS Homo sapiens.
XX  PN WO200153312-A1.
XX  PD 26-JUL-2001.
XX  XX 26-DEC-2000; 2000WO-US34263.
XX  PF 21-JAN-2000; 2000US-0488725.
XX  PR 25-APR-2000; 2000US-0552317.
XX  PR 09-JUL-2000; 2000US-0598042.
XX  PR 19-JUL-2000; 2000US-0620312.
XX  PR 03-AUG-2000; 2000US-0653450.
XX  PR 14-SEP-2000; 2000US-0662191.
XX  PR 19-OCT-2000; 2000US-0693036.
XX  PR 29-NOV-2000; 2000US-0727344.
XX  PA (HYSE-) HYSEQ INC.
XX  PI Tang YN, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX  PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX  PI Zhao QH, Zhou P, Goodrich R, Drmacic RT;
XX  DR WPI: 2001-442253/47.
XX  DR N-PSDB: AAI60583.
XX  PT Novel nucleic acids and polypeptides, useful for treating disorders
XX  PT such as central nervous system injuries -
XX  PS Example 2; SEQ ID NO 6358; 10078pp; English.
XX  CC The invention relates to human nucleic acids (AA157798-AA161369) and
XX  CC the encoded polypeptides (AAM38642-AAM42213) with nocotropic,
XX  CC immunosuppressant and cytostatic activity. The polynucleotides are useful
XX  CC in gene therapy. A composition containing a polypeptide or polynucleotide
XX  CC of the invention may be used to treat diseases of the peripheral nervous
XX  CC system, such as peripheral nervous injuries, peripheral neuropathy and
XX  CC localised neuropathies and central nervous system diseases, such as
XX  CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX  CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX  CC utilisation of the activities such as: Immune system suppression,
XX  CC activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic
XX  CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX  CC assays for receptor activity, arthritis and inflammation, leukaemias and
XX  CC C.N.S disorders.
XX  CC Note: The sequence data for this patent did not form part of the printed
XX  CC specification.
XX  SO Sequence 323 AA;
XX  Query Match 89.2%; Score 1385.5; DB 22; Length 323;
XX  Best Local Similarity 87.2%; Pred. No. 1.7e-153;
XX  Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
XX  QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHSKQISAEKQKGIIDCYVR 60
XX  I : I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
XX  26 MTEQAISFAKDFLAGGIAAASKTAVAPIERVKLLQVQHSKQIAADKQKGYIDCYVR 85
XX  DB 61 IPKEGGLSFWRGNLANVIRFPPTQALNFAFKDKYKQFLGVDNKHQFMRFFAGNLSG 120
XX  I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
XX  86 IPKEGGLSFWRGNLANVIRFPPTQALNFAFKDKYKQFLGVDNKHQFMRFFAGNLSG 145

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QY 121 GAAGATSLCFVYPLDFAFRTLRADVGR-AQREFHGLGDCIIRKFSKGLRGLYOGFNVS 179
 146 GAAGATSLCFVYPLDFAFRTLRADVGR-KSGEREFRLGDLVATKTSKGLRGLYOGFNVS 205
 QY 180 VGGIITIRAAVEGYDTAKGMLPDPKRVHIFVSMIAQSYTAVAGLSTPEPTVRRRM 239
 206 VGGIITIRAAVEGYDTAKGMLPDPKRVHIFVSMIAQSYTAVAGLSTPEPTVRRRM 265
 QY 240 QSGRKGADIMYTGTVDCKRKIADEGAKAFKFGKAMSNTLRGMCAPVLYLDEIKKYV 297
 266 QSGRKGADIMYTGTVDCKRKIFDEGKAFKFGKAMSNTLRGMCAPVLYLDEIKKYV 323
 Db
 RESULT 15
 ABG15423 standard; protein; 325 AA.
 ID ABG15423
 AC ABG15423;
 XX 18-FEB-2002 (first entry)
 XX Novel human diagnostic protein #15414.
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW Food supplement; medical imaging; diagnostic; genetic disorder.
 XX Homo sapiens.
 OS WO200175067-A2.
 PN 11-OCT-2001.
 PD 30-MAR-2001; 2001WO-0508631.
 PF 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 PA (HYSE-) HYSEQ INC.
 PI Drmanac RT, Liu C, Tang YT:
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS79610.
 XX
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PS Claim 20: SEQ ID No 45782; 103pp: English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 325 AA;
 Query Match 83.4%; Score 1294.5; DB 22; Length 325;
 Best Local Similarity 83.4%; Pred. No. 8e-143;
 Matches 251; Conservative 19; Mismatches 26; Indels 5; Gaps 4;
 QY 1 MGDHASFLLKDFLAGAFAAASVTAAVPIERVLLQVHASKQISAERKQKGIIDCV 60
 24 MTDAAVSFAKDFLAGGAAAIKSTAVAPIERVLLQVHASKQIADAKQKIIICV 83
 Db
 QY 61 IPKEGFLSFWRGNLANVIRYFPTQALNFAKDKYQLEFLGVDKHKQFWRFPAG 120
 84 IPKEGFLSFWRGNLANVIRYFPTQALNFAKDKYQLEFLGVDKHKQFWRFPAG 143
 Db
 QY 121 GAAGATSLCFVYPLDFAFRTLRADVGR-AQREFHGLGDCIIRKFSKGLRGLYOGFNVS 179
 144 GAAGATSLCFVYPLDFAFRTLRADVGR-KSGEREFRLGDLVATKTSKGLRGLYOGFNVS 203
 Db
 QY 180 VGGIITIRAAVEGYDTAKGMLPDPKRVHIFVSMIAQSYTAVAGLSTPEPTVRRRM 236
 204 VGGIITIRAAVEGYDTAKGMLPDPKRVHIFVSMIAQSYTAVAGLSTPEPTVRRRM 263
 Db
 QY 237 MMQSGRKGADIMYTGTVDCKRKIADEGAKAFKFGKAMSNTLRGMCAPVLYLDEIKKYV 295
 264 EXMQSGRKGADIMYTGTVDCKRKIADEGAKAFKFGKAMSNTLRGMCAPVLYLDEIKKYV 323
 Db
 QY 296 Y 296
 324 Y 324
 Db

Search completed: August 28, 2003, 19:38:47
 Job time : 53.2161 secs

RESULT 2
US-08-961-871-10
Sequence 10, Application US/08961871
Patent No. 6013858
GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: Macgregor, Grant R.
TITLE OF INVENTION: Mouse lacking Heart-Muscle Adenine
NUMBER OF INVENTION: Nucleotide Translocator Protein and Methods
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Feider, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-871-10
Query Match 93.9%; Score 1457.5; DB 3; Length 298;
Best Local Similarity 93.6%; Pred. No. 5.4e-161;
Matches 279; Conservative 10; Mismatches 8; Indels 1; Gaps 1;
QY 1 MGDHMSFLDPLAGAAVAAVSKTAVAPIERVKLLLOVHNSKQISAEKQYKGIIDCVR 60
DB 1 MGDALSLFLDPLAGAAVAAVSKTAVAPIERVKLLLOVHNSKQISAEKQYKGIIDCVR 60
QY 61 IPKQGLSTFWRGKLANVIRFPQALNFAFKDKYKQIFLGGVDKQRFYRFGNLSG 120
DB 61 IPKQGLSTFWRGKLANVIRFPQALNFAFKDKYKQIFLGGVDKQRFYRFGNLSG 120
QY 121 GAAGATSLCFVYPLDFARTRLADVGR-RAOREFHGLGDCIIFKFSKDGRLGLYQGFNV 179
DB 121 GAAGATSLCFVYPLDFARTRLADVGR-RAOREFHGLGDCIIFKFSKDGRLGLYQGFNV 180
QY 180 VQGIITIRAAVFGYDPAKGLPDPKRVHIFVSMIAQSVTAVALGLSTYPTDVRRRMM 239
DB 181 VQGIITIRAAVFGYDPAKGLPDPKRVHIFVSMIAQSVTAVALGLSTYPTDVRRRMM 240
QY 240 QSGRKGADIMYTGIVDCMRKIAKDEGAKAFKFGAMSVNLKMGCAFVLVLYDEIKKY 297
DB 241 QSGRKGADIMYTGIVDCMRKIAKDEGAKAFKFGAMSVNLKMGCAFVLVLYDEIKKY 298

RESULT 3
US-09-434-354-48

Sequence 48, Application US/09434354
Patent No. 6562563
GENERAL INFORMATION:
APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigert, Luciano G.
APPLICANT: Velicelbel, Gonul
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
FILE REFERENCE: 660088.433
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 48
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-434-354-48
Query Match 89.6%; Score 1391.5; DB 4; Length 298;
Best Local Similarity 88.6%; Pred. No. 2.5e-153;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
QY 1 MGDHMSFLDPLAGAAVAAVSKTAVAPIERVKLLLOVHNSKQISAEKQYKGIIDCVR 60
DB 1 MTDALSPFADPLAGAAVAAVSKTAVAPIERVKLLLOVHNSKQITADKQYKGIIDCVR 60
QY 61 IPKQGLSTFWRGKLANVIRFPQALNFAFKDKYKQIFLGGVDKQRFYRFGNLSG 120
DB 61 IPKQGLSTFWRGKLANVIRFPQALNFAFKDKYKQIFLGGVDKQRFYRFGNLSG 120
QY 121 GAAGATSLCFVYPLDFARTRLADVGR-RAOREFHGLGDCIIFKFSKDGRLGLYQGFNV 179
DB 121 GAAGATSLCFVYPLDFARTRLADVGR-RAOREFHGLGDCIIFKFSKDGRLGLYQGFNV 180
QY 180 VQGIITIRAAVFGYDPAKGLPDPKRVHIFVSMIAQSVTAVALGLSTYPTDVRRRMM 239
DB 181 VQGIITIRAAVFGYDPAKGLPDPKRVHIFVSMIAQSVTAVALGLSTYPTDVRRRMM 240
QY 240 QSGRKGADIMYTGIVDCMRKIAKDEGAKAFKFGAMSVNLKMGCAFVLVLYDEIKKY 296
DB 241 QSGRKGADIMYTGIVDCMRKIAKDEGAKAFKFGAMSVNLKMGCAFVLVLYDEIKKY 297
RESULT 4
US-09-434-354-49
Sequence 49, Application US/09434354
Patent No. 6562563
GENERAL INFORMATION:
APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigert, Luciano G.
APPLICANT: Velicelbel, Gonul
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
FILE REFERENCE: 660088.433
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 49
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien

US-09-434-354-49

Query Match	89.2%;	Score 1385.5;	DB 4;	Length 298;
Best Local Similarity	87.2%;	Pred. NO. 1.3e-152;		
Matches 260; Conservative	21;	Mismatches 16;	Indels 1;	Gaps 1.

[illegible]

RESULT 5
US-09-996-243-289

; Sequence 289, Application US/09996243
; Patent No. 6478825

GENERAL INFORMATION:

APPLICANT: Asnkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavyn, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secrected and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1c13
CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25

1	PRIOR APPLICATION NUMBER: 60/078910
2	PRIOR FILING DATE: 1998-03-20
3	PRIOR APPLICATION NUMBER: 60/08333222
4	PRIOR FILING DATE: 1998-04-28
5	PRIOR APPLICATION NUMBER: 60/084600
6	PRIOR FILING DATE: 1998-05-07
7	PRIOR APPLICATION NUMBER: 60/087106
8	PRIOR FILING DATE: 1998-05-28
9	PRIOR APPLICATION NUMBER: 60/087607
10	PRIOR FILING DATE: 1998-06-02
11	PRIOR APPLICATION NUMBER: 60/087609
12	PRIOR FILING DATE: 1998-06-02
13	PRIOR APPLICATION NUMBER: 60/087759
14	PRIOR FILING DATE: 1998-06-02
15	PRIOR APPLICATION NUMBER: 60/087827
16	PRIOR FILING DATE: 1998-06-03
17	PRIOR APPLICATION NUMBER: 60/088021
18	PRIOR FILING DATE: 1998-06-04
19	PRIOR APPLICATION NUMBER: 60/088025
20	PRIOR FILING DATE: 1998-06-04
21	PRIOR APPLICATION NUMBER: 60/088026
22	PRIOR FILING DATE: 1998-06-04
23	PRIOR APPLICATION NUMBER: 60/088028
24	PRIOR FILING DATE: 1998-06-04
25	PRIOR APPLICATION NUMBER: 60/088029
26	PRIOR FILING DATE: 1998-06-04
27	PRIOR APPLICATION NUMBER: 60/088030
28	PRIOR FILING DATE: 1998-06-04
29	PRIOR APPLICATION NUMBER: 60/088033
30	PRIOR FILING DATE: 1998-06-04
31	PRIOR APPLICATION NUMBER: 60/088328
32	PRIOR FILING DATE: 1998-06-04
33	PRIOR APPLICATION NUMBER: 60/088167
34	PRIOR FILING DATE: 1998-06-05
35	PRIOR APPLICATION NUMBER: 60/088202
36	PRIOR FILING DATE: 1998-06-05
37	PRIOR APPLICATION NUMBER: 60/088212
38	PRIOR FILING DATE: 1998-06-05
39	PRIOR APPLICATION NUMBER: 60/088217
40	PRIOR FILING DATE: 1998-06-05
41	PRIOR APPLICATION NUMBER: 60/088655
42	PRIOR FILING DATE: 1998-06-09
43	PRIOR APPLICATION NUMBER: 60/088734
44	PRIOR FILING DATE: 1998-06-10
45	PRIOR APPLICATION NUMBER: 60/088738
46	PRIOR FILING DATE: 1998-06-10
47	PRIOR APPLICATION NUMBER: 60/088742
48	PRIOR FILING DATE: 1998-06-10
49	PRIOR APPLICATION NUMBER: 60/088810
50	PRIOR FILING DATE: 1998-06-10
51	PRIOR APPLICATION NUMBER: 60/088824
52	PRIOR FILING DATE: 1998-06-10
53	PRIOR APPLICATION NUMBER: 60/088826
54	PRIOR FILING DATE: 1998-06-10
55	PRIOR APPLICATION NUMBER: 60/088876
56	PRIOR FILING DATE: 1998-06-11
57	PRIOR APPLICATION NUMBER: 60/088876
58	PRIOR FILING DATE: 1998-06-11
59	PRIOR APPLICATION NUMBER: 60/089105
60	PRIOR FILING DATE: 1998-06-12
61	PRIOR APPLICATION NUMBER: 60/089440
62	PRIOR FILING DATE: 1998-06-16
63	PRIOR APPLICATION NUMBER: 60/089512
64	PRIOR FILING DATE: 1998-06-16
65	PRIOR APPLICATION NUMBER: 60/089514
66	PRIOR FILING DATE: 1998-06-16
67	PRIOR APPLICATION NUMBER: 60/089533
68	PRIOR FILING DATE: 1998-06-17
69	PRIOR APPLICATION NUMBER: 60/089538
70	PRIOR FILING DATE: 1998-06-17
71	PRIOR APPLICATION NUMBER: 60/089596

PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
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PRIOR FILING DATE: 1998-06-22
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PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090445
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
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PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
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PRIOR FILING DATE: 1998-06-25
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 19.6%; Score 304; DB 4; Length 469;
Best Local Similarity 29.0%; Pred. No. 1,4e-26;
Matches 88; Conservative 58; Mismatches 115; Indels 42; Gaps 11;

QY 6 WSLFKDFLAGAANAASKTAVAPIERVKLLLOVHASKOISAKOYKGIIDCVRIKPEQ 65
DB 187 WRHL---VAGCGAGANSRITCTAPDLRLKVLMOV-HASR-----SNMKGIYCGFTOMIREG 237
QY 66 GFLSPWGRNLANYIRYFPTQALNFAFKDKYKQDLFGVDH-----HKQFRRYFAGNLIASC 120
DB 238 GARSLSWNGINIVLKIAPESAIKFMAYEQIKRLV--GSDQETLRIHER-----LVAG 287
QY 121 GAAGATSLCFVYPLDPAKRTLADVGRRAOREHGLDCTIKIKFKSDGLGLYQGFNVSV 180
DB 288 SLAGAIAOSSIVPEVETKTMAL---RKTGQYSGMLDCARRILAREGVAFAFKGYVPM 343
QY 181 OGIIYRAAFYGYDTAKGM-----LPPKRVHIFVSMIAQSVTAVAGLSTPFD 232
DB 344 LGIIPYAGIDLAVERLKNMLOHYAVNSADP---GVFYLLACGTSSTSCGQASLPFLAL 400
QY 233 VRRMMQSGRKADIMYGTVDWCRIANDEGAKAFKFGAMSVLRGMGAFV-LVLD 291
DB 401 VTRMQAQSISGAPEVTMSL--FKHILTEGAFGLYRLADPNFMKVIPAVSISYVYE 458
QY 292 EIK 294
DB 459 NLR 461

RESULT 6
US-09-188-930-339
Sequence 339, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 469
TYPE: PRT
ORGANISM: Mouse
US-09-188-930-339

Query Match 19.4%; Score 301; DB 3; Length 469;
Best Local Similarity 28.9%; Pred. No. 3e-26;
Matches 89; Conservative 64; Mismatches 103; Indels 52; Gaps 14;

QY 6 WSLFKDFLAGAANAASKTAVAPIERVKLLLOVHASKOISAKOYKGIIDCV---RI 61
DB 187 WRHL---VAGCGAGANSRITCTAPDLRLKVLMOV-HASRNNM-----CIVGFTQM 233
QY 62 PKQGLSPWGRNLANYIRYFPTQALNFAFKDKYKQDLFGVDH-----HKQFRRYFAGN 116


```

: RESULT 10
: US-09-501-558-2
: Sequence 2, Application US/09501558
: Patent No. 6403784
: GENERAL INFORMATION:
: APPLICANT: Turner, C. Alexander Jr.
: APPLICANT: Machur, Brian
: APPLICANT: Zambrowicz, Brian
: APPLICANT: Sands, Arthur T.
: TITLE OF INVENTION: No. 6403784el Human Uncoupling Proteins and
: TITLE OF INVENTION: Polynucleotides Encoding the Same
: FILE REFERENCE: LEX-0012-USA
: CURRENT APPLICATION NUMBER: US/09/501,558
: CURRENT FILING DATE: 2000-02-09
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 291
: TYPE: PR1
: ORGANISM: Homo sapiens
: US-09-501-558-2

```

```

: Sequence 118 Application US/09482273
: Patent No. 6534631
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: 71 Human Secreted Proteins
: FILE REFERENCE: P2030P1
: CURRENT APPLICATION NUMBER: US/09/482,273
: CURRENT FILING DATE: 2000-01-13
: EARLIER APPLICATION NUMBER: PCT/US99/15849
: EARLIER FILING DATE: 1999-07-14
: EARLIER APPLICATION NUMBER: 60/092,921
: EARLIER FILING DATE: 1998-07-15
: EARLIER APPLICATION NUMBER: 60/092,922
: EARLIER FILING DATE: 1998-07-15
: EARLIER APPLICATION NUMBER: 60/092,956
: EARLIER FILING DATE: 1998-07-15
: NUMBER OF SEQ ID NOS: 267
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO: 118
: LENGTH: 335
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (335)
: OTHER INFORMATION: xaa equals stop translation
:
: US-09-482-273-118
:
: Query Match 17.1%; Score 265.5; DB 4; Length 335;
: Best Local Similarity 30.0%; Pred. No. 2.4e-22;
: Matches 89; Conservative 43; Mismatches 138; Indels 27; Gaps 10;
:
: QY 10 KDELAGAANAASKEVTAVAPIERVKLLDVOHASKOISA---EKQYKGIIDCVVPIPEQG 66
: | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: 51 KPEVYGGSLAVAEFGFPPDLTKTRIQV--GQSIDARRKEIKYRGMFALPRICKEG 108
:
: QY 67 FLSEFRGNLANVIRYPTQALNFAKDKYQLFLGVDRHKQRMRYFAGMLASGAAGAT 126
: | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: 109 VALAYSGIAFALRKQASVGTIKIGIYOSLRLF---VERLED--ETLLIMICGVSGVI 163
:
: QY 127 SLCEVYPLDEAFATRLADVBRRAQRERHGLGDCIIRKFSKSDGLRGVGFNVSGVGIIT 186
: | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: 164 SSTIANPTDYLKTRIMQAO--GSLFQSGMIG--SFIDYQDEGTGLRWGVPTIQRAAIV 219
:
: Db 187 RAAFGVYDTAK-----GNLPDPKKNHIFVSMNIAQSVYAVAG--LLSYFPDVRRRMM 239
: | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: 220 VGVELPYVDITKHKHLILSGMMGDFILNH-----FVSEFTGGLAGALASNPDVVRTBMN 274
:
: QY 240 QSGRGKADINVTGTVDCKRKIAKDEGAKAFKFGAMSVLR--GMGAFVLYLYDEIKR 295
: | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: 275 QRAIVGHVDLYKGTVDGILKMKRHEGFFALYKGFWPMWRLGPMNIIFETIYEQDKR 331
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:
: RESULT 12
: US-08-933-750C-12
: Sequence 12, Application US/08933750C
: Patent No. 5932442
: GENERAL INFORMATION:
: APPLICANT: Lal, Preeti
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Bandman, Olga
: APPLICANT: Shah, Puryi
: APPLICANT: Au-Young, Janice
: APPLICANT: Yue, Henry
: APPLICANT: Guegler, Karl J.
: APPLICANT: Corley, Neil C.
: TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
: NUMBER OF SEQUENCES: 98
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA

```

```

COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SPINNOT02
CLONE: 207452
US-08-933-750C-12

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Query Match	15.3%	Score 238	DB 2:	Length 320:
Best Local Similarity	23.5%	Pred. No.	3.6e-19:	
Matches 71:	Conservative 67:	Mismatches 124:	Indels 40:	Gaps 10

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Db      20 VAGSVSGLYTRALISFPVDYIKIRPOLQHRRLSRSPSKKYTGILLIOASHOILIDEGGPRAFW 79
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      72 RGLMANVIREFPTOLNF-AFKDKYKOLEFLGVDRHKOFRMYFAGNLSAAGAAGATSLCF 130Z
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Db      80 KGHVPKOLLISIGVANOFELSFEMLTETHRGVSUYDAREFSVHF-----VCGGLACMAMTLT 135Z
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      131 VFELDPARTLADYVGRAROREFHGLDGOCIIIFKPSDLRGLXOGFNVSVOGIIITYAAAY 190Z
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      136 VHEVDVLRTREFAA--QGEPKYYNTLRNAVGMYSBEOVFYTKGLAPTLAIFFPYGLQ 192Z
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      191 FGYITDAKMPLDPKNHIIFSVMTI-----AQSTAVAGLLSYFDFTVR 235Z
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      193 FSCYSYLK-----HLV-KMALPRABEKKNNENLOMLCDSGAGVISKTLTYPLDIIEFKK 242Z
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OY      236 RMMA--QSGRK--GADIWYTGTVCMMIRIADEGAKAFPGAGSNVLR--OMGAPFVLVL 289Z
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      243 RLQVGGEFHARAARAFQVRRYRKGMLDMCAQVLOJKEBALFFFGGLBSLTKALSLSTGFVFFS 302Z
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      290 YD 291
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Db      303 YE 304

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RESULT 13
US-09-234-613-12
Sequence 12, Application US/09234613
Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yee, Henry

1 APPLICANT: Guegler, Karl J.
2 APPLICANT: Corley, Neil C.
3 TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
4 NUMBER OF SEQUENCES: 98
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: Incyte Pharmaceuticals, Inc.
7 STREET: 3174 Porter Drive
8 CITY: Palo Alto
9 STATE: CA
10 COUNTRY: USA
11 ZIP: 94304
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Diskette
14 COMPUTER: IBM Compatible
15 OPERATING SYSTEM: DOS
16 SOFTWARE: FASTSEQ for Windows Version 2.0
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/09/234,613
19 FILING DATE:
20 CLASSIFICATION:
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US/08/933,750
23 FILING DATE: September 23, 1997
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Billings, Lucy J.
26 REGISTRATION NUMBER: 36,749
27 REFERENCE/DOCKET NUMBER: PF-0356 US
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: 415-855-0555
30 TELEFAX: 415-845-4166
31 TELEX:
32 INFORMATION FOR SEQ ID NO: 12:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 320 amino acids
35 TYPE: amino acid
36 STRANDEDNESS: single
37 TOPOLOGY: linear
38 IMMEDIATE SOURCE:
39 LIBRARY: SPINNOT02
40 CLONE: 207452
41 US-09-234-613-12

Query Match	15.3%	Score 238	DB 3	Length 320
Best Local Similarity	23.5%	Pred. No. 3.6e-19		
Matches 71; Conservative	67;	Mismatches 124;	Indels 40;	Gaps 10

[illegible]

RESULT 14
US-09-142-565-2

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: Sequence 2, Application US/09142565A
: Patent No. 6187560
:
: GENERAL INFORMATION:
: APPLICANT: Lee James Beeley
: APPLICANT: Kelly Paine
: APPLICANT: Robert James
: TITLE OF INVENTION: NOVEL COMPOUNDS
: FILE REFERENCE: GH-30002
: CURRENT APPLICATION NUMBER: US/09/142,565A
: CURRENT FILING DATE: 1999-06-30
: EARLIER APPLICATION NUMBER: 9704551.2
: EARLIER FILING DATE: 1997-03-05
: EARLIER APPLICATION NUMBER: 9705614.7
: EARLIER FILING DATE: 1997-03-18
: EARLIER APPLICATION NUMBER: 97305305.1
: EARLIER FILING DATE: 1997-07-16
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 312
: TYPE: prt
: ORGANISM: HOMO SAPIEN
: US-09-142-565-2

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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
JN-08-518-878B-56

Query Match	14.68	Score 227	DB 1	Length 299
Best Local Similarity	23.88	Pred. NO. 6.2e-18		
Matches 70	Conservative 52	Mismatches 148	Indels 24	Gaps 7

Search completed: August 28, 2003, 19:44:18
Job time : 19.9597 secs

RESULT 15
US-08-518-8788-56
Sequence 56, Application US/08518878B
Patent No. 5702902
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,878B
FILING DATE: 23-AUG-1995

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: August 28, 2003, 19:38:56 ; Search time 19.29 Seconds

(Without alignments)
2105.969 Million cell updates/sec

Title: US-09-811-132-31

Perfect score: 1553
Sequence: 1 MGDHMSFLKDFLAGAATAA.....LRGNGAFVLYLDEIRKVV 297

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 510680 seqs, 136781880 residues

Total number of hits satisfying chosen parameters: 510680

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09C_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1553	100.0	297	US-09-811-094-31	Sequence 31, Appl
2	1553	100.0	297	US-09-810-644-31	Sequence 31, Appl
3	1553	100.0	297	US-09-185-904A-31	Sequence 31, Appl
4	1391.5	89.6	298	US-09-811-094-32	Sequence 32, Appl
5	1391.5	89.6	298	US-09-810-644-32	Sequence 32, Appl
6	1391.5	89.6	298	US-09-185-904A-32	Sequence 32, Appl
7	1385.5	89.2	298	US-09-811-094-33	Sequence 33, Appl
8	1385.5	89.2	298	US-09-810-644-33	Sequence 33, Appl
9	1385.5	89.2	298	US-09-185-904A-33	Sequence 33, Appl
10	740	47.6	381	US-10-141-478A-2	Sequence 2, Appl
11	734	47.3	318	US-09-801-368-252	Sequence 252, Appl
12	734	47.3	386	US-09-734-569-170	Sequence 170, Appl
13	703.5	45.3	308	US-10-128-714-3338	Sequence 3338, Appl
14	703.5	45.3	308	US-10-128-714-8338	Sequence 8338, Appl
15	666	42.9	12	US-10-259-165-192	Sequence 192, Appl

16	461	29.7	132	9	US-09-925-301-1459	Sequence 1459, Appl
17	402.5	25.9	87	9	US-09-864-761-36440	Sequence 36440, A
18	350.5	22.6	475	10	US-09-777-921A-4	Sequence 4, Appl
19	346.5	22.3	477	10	US-09-777-921A-2	Sequence 2, Appl
20	312	20.1	410	10	US-09-777-921A-5	Sequence 5, Appl
21	304	19.6	469	9	US-09-989-722-289	Sequence 289, Appl
22	304	19.6	469	9	US-09-989-723-289	Sequence 289, Appl
23	304	19.6	469	9	US-09-989-279-289	Sequence 289, Appl
24	304	19.6	469	9	US-09-989-727-289	Sequence 289, Appl
25	304	19.6	469	10	US-09-989-731-289	Sequence 289, Appl
26	304	19.6	469	10	US-09-989-732-289	Sequence 289, Appl
27	304	19.6	469	10	US-09-991-073-289	Sequence 289, Appl
28	304	19.6	469	10	US-09-990-442-289	Sequence 289, Appl
29	304	19.6	469	10	US-09-991-163-289	Sequence 289, Appl
30	304	19.6	469	10	US-09-993-604-289	Sequence 289, Appl
31	304	19.6	469	10	US-09-990-456-289	Sequence 289, Appl
32	304	19.6	469	10	US-09-989-721-289	Sequence 289, Appl
33	304	19.6	469	10	US-09-992-588-289	Sequence 289, Appl
34	304	19.6	469	10	US-09-989-293A-289	Sequence 289, Appl
35	304	19.6	469	10	US-09-989-735-289	Sequence 289, Appl
36	304	19.6	469	10	US-09-990-444-289	Sequence 289, Appl
37	304	19.6	469	10	US-09-991-181-289	Sequence 289, Appl
38	304	19.6	469	10	US-09-989-730-289	Sequence 289, Appl
39	304	19.6	469	10	US-09-990-436-289	Sequence 289, Appl
40	304	19.6	469	10	US-09-993-687-289	Sequence 289, Appl
41	304	19.6	469	11	US-09-989-734-289	Sequence 289, Appl
42	304	19.6	469	11	US-09-997-653-289	Sequence 289, Appl
43	304	19.6	469	11	US-09-993-667-289	Sequence 289, Appl
44	304	19.6	469	11	US-09-997-428-289	Sequence 289, Appl
45	304	19.6	469	11	US-09-997-666-289	Sequence 289, Appl

ALIGNMENTS

RESULT 1
US-09-811-094-31
; Sequence 31, Application US/09811094
; Patent No. US20010044144A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willet, Scott W.
; APPLICANT: Szabo, Thomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yezhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-811-094-31
Query Match 100.0% Score 1553; DB 9; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.3e-160;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 MGDHMSFLKDFLAGAATAAASKTAVAPIERKLLIQVHASKQISAERQYGIIDCYVR 60
|||||
1 IKDEGFLSWGNANTYIRFPQALNFAFDKQKQFLGVDNRHKKQFWRYFAGNLSAG 120
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61 IKDEGFLSWGNANTYIRFPQALNFAFDKQKQFLGVDNRHKKQFWRYFAGNLSAG 120
|||||
61 IKDEGFLSWGNANTYIRFPQALNFAFDKQKQFLGVDNRHKKQFWRYFAGNLSAG 120
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Oy	121	GAAGATSLCEVYVLPDAPFRRLAADVGRRAQREHGLGCIIKIPFSDGLRGLYGFNVSV	180
	121	GAAGATSLCEVYVLPDAPFRRLAADVGRRAQREHGLGCIIKIPFSDGLRGLYGFNVSV	180
Oy	181	OGIIITYRAALFEGVYDTAKMLPDPKKNVHLEWSMLIAQSVTAAGLLSYPEFDVRRRMQ	240
	181	OGIIITYRAALFEGVYDTAKMLPDPKKNVHLEWSMLIAQSVTAAGLLSYPEFDVRRRMQ	240
Oy	241	SGRGKADIMYTGVDQWRKLIARDDEGAKAFKAGAMSNVLRGGAFLVLYLDELIRKYV	297
	241	SGRGKADIMYTGVDQWRKLIARDDEGAKAFKAGAMSNVLRGGAFLVLYLDELIRKYV	297

RESULT 2
 US-09-810-644-31
 : Sequence 31, Application US/09810644
 : Patent No. US20020012892A1

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RESULT 2
US-09-810-644-31
: Sequence 31, Application US/09810644
: Patent No. US20020012992A1
: GENERAL INFORMATION:
: APPLICANT: Anderson, Christen M.
: APPLICANT: Davis, Robert E.
: APPLICANT: Clevenger, William
: APPLICANT: Wiley, Sandra Ellen
: APPLICANT: Waller, Scott W.
: APPLICANT: Szabo, Tomas R.
: APPLICANT: Ghosh, Soumitra S.
: APPLICANT: Moos, Walter H.
: APPLICANT: Pel, Yashong
: TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT)
: TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
: FILE REFERENCE: 660088.42D03
: CURRENT APPLICATION NUMBER: US/09/810,644
: CURRENT FILING DATE: 2001-03-14
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 31
: LENGTH: 297
: TYPE: PR1
: ORGANISM: Homo sapien
: US-09-810-644-31

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Query Match	100.0% ;	Score 1553 ;	DB 9 ;	Length 297 ;
Best Local Similarity	100.0% ;	Pred. No. 1,3e-160 ;		
Matches 297 ;	Conservative 0 ;	Mismatches 0 ;	Indels 0 ;	Gaps 0
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Db	1	MGHANSFLKDFLAGVAAAASVKTAVAPIERKYLLOVQHASKOISAEKQTKGIIIDCVR	60	
QY	61	IPKEGQFLSFWRKGNLANVIRYPTGALNFAFDKTKQLEFGVDRHQAQFMFYFAGNLSG	120	
Db	61	IPKEGQFLSFWRKGNLANVIRYPTGALNFAFDKTKQLEFGVDRHQAQFMFYFAGNLSG	120	
QY	121	GAAGATSLCFYYPIDPFAKRLAADYGRRAQREFFGLDCLIKFKSDGLKLTQGFENVSY	180	
Db	121	GAAGATSLCFYYPIDPFAKRLAADYGRRAQREFFGLDCLIKFKSDGLKLTQGFENVSY	180	
QY	181	QGIIIRAAVFCGYDTAKGMLDPDPKNVNI FVSWMIAQSVTAAGLLSYPEDEVRRMMQ	240	
Db	181	QGIIIRAAVFCGYDTAKGMLDPDPKNVNI FVSWMIAQSVTAAGLLSYPEDEVRRMMQ	240	
QY	241	SGRKGADIMYTGIVDCMKRIADDEAKAFPFKGANSNVLKRGKGFVLYLDELKKYV	297	
Db	241	SGRKGADIMYTGIVDCMKRIADDEAKAFPFKGANSNVLKRGKGFVLYLDELKKYV	297	

RESULT3
US-09-185-904A-31
Sequence 31, Application US/09185904A
Patent No. US20020177185A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.

```

1  APPLICANT: Cleveland, William
2  APPLICANT: Wiley, Sandra Eileen
3  APPLICANT: Miller, Scott W.
4  APPLICANT: Szabo, Tomas R.
5  APPLICANT: Ghosh, Soumitra S.
6  TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
7  TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
8  TITLE OF INVENTION: THEREFOR
9  FILE REFERENCE: 660088.420
10 CURRENT APPLICATION NUMBER: US/09/185,904A
11 CURRENT FILING DATE: 1998-11-03
12 NUMBER OF SEQ ID NOS: 33
13 SOFTWARE: FastSeq for Windows Version 3.0
14 SEQ ID NO 31
15 LENGTH: 297
16 TYPE: PRT
17 ORGANISM: Homo sapien
18 US-09-185-904A-31

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Query Match	100.0%;	Score 1553;	DB 10;	Length 297;																																																	
Best Local Similarity	100.0%;	Pred. No. 1,3e-160;																																																			
Matches	297;	Conservative	0;	Mismatches	0;																																																
				Indels	0;																																																
				Gaps	0																																																
QY	1	MGDHASF	LKD	FLG	AAVAAVSK	TA	VA	DI	ERV	KLL	LQ	VO	H	SK	Q	S	K	O	I	S	A	E	K	O	Y	K	G	I	I	D	C	V	R	60																			
Db	1	MGDHASF	LKD	FLG	AAVAAVSK	TA	VA	DI	ERV	KLL	LQ	VO	H	SK	Q	S	A	E	K	O	I	S	A	E	K	O	Y	K	G	I	I	D	C	V	R	60																	
QY	61	IPKRG	F	SE	FR	G	N	L	A	N	I	R	F	P	O	A	L	F	A	F	K	D	K	O	L	F	G	V	D	H	K	O	F	M	R	E	A	G	N	L	A	S	G	120									
Db	61	IPKRG	F	SE	FR	G	N	L	A	N	I	R	F	P	O	A	L	F	A	F	K	D	K	O	L	F	G	V	D	H	K	O	F	M	R	E	A	G	N	L	A	S	G	120									
QY	121	GAA	A	T	S	C	E	F	Y	P	I	D	F	A	R	T	L	A	A	D	V	G	R	A	O	R	E	F	H	G	L	G	C	I	I	K	E	F	S	D	G	L	R	G	L	Y	O	G	F	N	S	V	180
Db	121	GAA	A	T	S	C	E	F	Y	P	I	D	F	A	R	T	L	A	A	D	V	G	R	A	O	R	E	F	H	G	L	G	C	I	I	K	E	F	S	D	G	L	R	G	L	Y	O	G	F	N	S	V	180
QY	181	Q	G	I	I	T	R	A	A	Y	G	V	D	T	A	K	G	M	L	P	D	R	E	N	V	I	F	S	M	I	A	I	S	V	T	A	V	A	G	L	S	T	P	E	D	I	V	R	R	M	M	Q	240
Db	181	Q	G	I	I	T	R	A	A	Y	G	V	D	T	A	K	G	M	L	P	D	R	E	N	V	I	F	S	M	I	A	I	S	V	T	A	V	A	G	L	S	T	P	E	D	I	V	R	R	M	M	Q	240
QY	241	S	G	R	G	A	D	I	M	T	G	V	D	C	M	R	K	I	A	K	D	E	A	R	K	F	E	F	G	A	M	S	N	T	R	G	M	G	A	V	L	V	L	Y	D	E	I	K	T	Y	297		
Db	241	S	G	R	G	A	D	I	M	T	G	V	D	C	M	R	K	I	A	K	D	E	A	R	K	F	E	F	G	A	M	S	N	T	R	G	M	G	A	V	L	V	L	Y	D	E	I	K	T	Y	297		

RESULT 4
US-09-811-094-32
Sequence 32. Application US/09811094
Patent No. US20010044144n1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yezhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT'),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.42004
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ. ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0

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; LENGTH: 298
; TYPE: PRT
; ORGNISM: Homo sapien
US-09-811-094-32
Query Match      89.6%; Score 1391.5; DB 9; Length 298;
Best Local Similarity 88.6%; Pred. No. 5e-143;

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Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLLOVHASKOISAEKQKGIIDCYVR 60
 DB 1 MTDAAISFAKDFLAGVAANAISKTAVAPIERVKLLLOVHASKOITADKQKGIIDCYVR 60
 QY 61 IPKQGLSFWRGNLANVIRFPFOALNFAFKDKYKQFLGVDNRHKOFRWYFAGNLSG 120
 DB 61 IPKQGLSFWRGNLANVIRFPFOALNFAFKDKYKQFLGVDNRHKOFRWYFAGNLSG 120
 QY 121 GAAGATSLCFYYPDPDFARTLAADYGR- AOREFHGLDCLTIKIKSGSLGKLYOGFNVS 179
 DB 121 GAAGATSLCFYYPDPDFARTLAADYGR- AOREFHGLDCLTIKIKSGSLGKLYOGFNVS 180
 QY 180 VOGIIIRAAAYFGYIDTAAGMLPDPKNVHIFVSMIAQSVTAVALGSLYPEDTVARRMM 239
 DB 181 VOGIIIRAAAYFGYIDTAAGMLPDPKNVHIFVSMIAQSVTAVALGSLYPEDTVARRMM 240
 QY 240 QSGRKGADIMYTGIVDCWRKIAKDEGAKAFKFGAMSNVLRGNGAFVLVLYDEIKKY 296
 DB 241 QSGRKGADIMYTGIVDCWRKIAKDEGAKAFKFGAMSNVLRGNGAFVLVLYDEIKKY 297

RESULT 5

US-09-810-644-32
 ; Sequence 32, Application US/09810644
 ; Patent No. US20020012992A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.
 ; APPLICANT: Clevenger, William
 ; APPLICANT: Wiley, Sandra Eileen
 ; APPLICANT: Szabo, Tomas R.
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Moos, Walter H.
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
 ; FILE REFERENCE: 660088.420D3
 ; CURRENT APPLICATION NUMBER: US/09/810.644
 ; CURRENT FILING DATE: 2001-03-14
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 32
 ; LENGTH: 298
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-810-644-32

Query Match 89.6%; Score 1391.5; DB 9; Length 298;
 Best Local Similarity 88.6%; Pred. No. 5e-143;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLLOVHASKOISAEKQKGIIDCYVR 60
 DB 1 MTDAAISFAKDFLAGVAANAISKTAVAPIERVKLLLOVHASKOITADKQKGIIDCYVR 60
 QY 61 IPKQGLSFWRGNLANVIRFPFOALNFAFKDKYKQFLGVDNRHKOFRWYFAGNLSG 120
 DB 61 IPKQGLSFWRGNLANVIRFPFOALNFAFKDKYKQFLGVDNRHKOFRWYFAGNLSG 120
 QY 121 GAAGATSLCFYYPDPDFARTLAADYGR- AOREFHGLDCLTIKIKSGSLGKLYOGFNVS 179
 DB 121 GAAGATSLCFYYPDPDFARTLAADYGR- AOREFHGLDCLTIKIKSGSLGKLYOGFNVS 180
 QY 180 VOGIIIRAAAYFGYIDTAAGMLPDPKNVHIFVSMIAQSVTAVALGSLYPEDTVARRMM 239
 DB 181 VOGIIIRAAAYFGYIDTAAGMLPDPKNVHIFVSMIAQSVTAVALGSLYPEDTVARRMM 240
 QY 240 QSGRKGADIMYTGIVDCWRKIAKDEGAKAFKFGAMSNVLRGNGAFVLVLYDEIKKY 296
 DB 241 QSGRKGADIMYTGIVDCWRKIAKDEGAKAFKFGAMSNVLRGNGAFVLVLYDEIKKY 297

RESULT 6

US-09-185-904A-32
 ; Sequence 32, Application US/09185904A
 ; Patent No. US20020177185A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.
 ; APPLICANT: Clevenger, William
 ; APPLICANT: Wiley, Sandra Eileen
 ; APPLICANT: Szabo, Tomas R.
 ; APPLICANT: Ghosh, Soumitra S.
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
 ; FILE REFERENCE: 660088.420
 ; CURRENT APPLICATION NUMBER: US/09/185.904A
 ; CURRENT FILING DATE: 1998-11-03
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 32
 ; LENGTH: 298
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-185-904A-32

Query Match 89.6%; Score 1391.5; DB 10; Length 298;
 Best Local Similarity 88.6%; Pred. No. 5e-143;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLLOVHASKOISAEKQKGIIDCYVR 60
 DB 1 MTDAAISFAKDFLAGVAANAISKTAVAPIERVKLLLOVHASKOITADKQKGIIDCYVR 60
 QY 61 IPKQGLSFWRGNLANVIRFPFOALNFAFKDKYKQFLGVDNRHKOFRWYFAGNLSG 120
 DB 61 IPKQGLSFWRGNLANVIRFPFOALNFAFKDKYKQFLGVDNRHKOFRWYFAGNLSG 120
 QY 121 GAAGATSLCFYYPDPDFARTLAADYGR- AOREFHGLDCLTIKIKSGSLGKLYOGFNVS 179
 DB 121 GAAGATSLCFYYPDPDFARTLAADYGR- AOREFHGLDCLTIKIKSGSLGKLYOGFNVS 180
 QY 180 VOGIIIRAAAYFGYIDTAAGMLPDPKNVHIFVSMIAQSVTAVALGSLYPEDTVARRMM 239
 DB 181 VOGIIIRAAAYFGYIDTAAGMLPDPKNVHIFVSMIAQSVTAVALGSLYPEDTVARRMM 240
 QY 240 QSGRKGADIMYTGIVDCWRKIAKDEGAKAFKFGAMSNVLRGNGAFVLVLYDEIKKY 296
 DB 241 QSGRKGADIMYTGIVDCWRKIAKDEGAKAFKFGAMSNVLRGNGAFVLVLYDEIKKY 297

RESULT 7

US-09-811-094-33
 ; Sequence 33, Application US/09811094
 ; Patent No. US20010044144A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.
 ; APPLICANT: Clevenger, William
 ; APPLICANT: Wiley, Sandra Eileen
 ; APPLICANT: Szabo, Tomas R.
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Moos, Walter H.
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
 ; FILE REFERENCE: 660088.420D4
 ; CURRENT APPLICATION NUMBER: US/09/811.094
 ; CURRENT FILING DATE: 2001-03-14
 ; NUMBER OF SEQ ID NOS: 37

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: SOFTWARE: PastSeq for Windows Version 3.0
: SER ID NO 33
: LENGTH: 298
: TYPE: PRT
: ORGANISM: Homo sapien
US-09-811-094-33

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Query Match	89.28;	Score 1385.5;	DB 9;	length 298;
Best Local Similarity	87.28;	Pred. No. 2.3e-142;		
Matches 260;	Conservative 21;	Mismatches 16;	Indels 1;	Gaps 1

[illegible]

```

RESULT 8
US-09-810-644-33
? Sequence 33, Application US/09810644
? Patent No. US20020012992A1
?
GENERAL INFORMATION:
?
? APPLICANT: Anderson, Christen M.
? APPLICANT: Davis, Robert E.
? APPLICANT: Clevenger, William
? APPLICANT: Wiley, Sandra Eileen
? APPLICANT: Miller, Scott W.
? APPLICANT: Szabo, Tomas R.
? APPLICANT: Ghosh, Soumitra S.
? APPLICANT: Moos, Walter H.
? APPLICANT: Pel, Yashong
?
? TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT'),
? FILE REFERENCE: 660088, 420D3
? CURRENT APPLICATION NUMBER: US/09/810,644
? CURRENT FILING DATE: 2001-03-14
?
? NUMBER OF SEQ ID NOS: 37
? SOFTWARE: FastSeq for Windows Version 3.0
?
? SEQ ID NO 33
? LENGTH: 298
? TYPE: PRT
? ORGANISM: Homo sapien
US-09-810-644-33

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[illegible]

Db	121	GAGAAATSLFEVYPLDEAFRLAADYKGSSTEEFEFGLCDLVRITTKSDGJINGLYQGSFVS	180
Qy	180	VGGIIITRYPAAYEGVDYDTAKGMLPDRNNVHIFSMIAQSYAAVAGLLSYEPDPTRRMM	239
Db	181	VGGIIITRYPAAYEGVDYDTAKGMLPDRNNHIVSMIAQTYTAAVAGVSYEPDPTRRMM	240
Qy	240	QSGRKADIMYGTUYDCMKRIAKDGAARFEGASNNLRMGCAFVLYLYDEKTKV	297
Db	241	QSGRKADIMYGTUYDCMKRIKRDGGAARFEGASNNLRMGCAFVLYLYDEKTKV	298

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RESULT 9
US-09-185-904A-33
; Sequence 33, Application US/09185904A
; Patent No. US2002017183A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Wiley, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
; TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 660088.420
; CURRENT APPLICATION NUMBER: US/09/185,904A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 298
; TYPE: PRF
; ORGANISM: Homo sapien
US-09-185-904A-33

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Query Match      89.2%; Score 1385.5; DB 10; Length 298;
Best Local Similarity 87.2%; Pred. No. 2,3=142;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY      1 MGDHMSFLDELTAAGAAAAYSKTAVAPIERVKLLLOVQHASKOISAEKQYKGIIDCYVR 60
      1 MTEQAIISFADFDLGGIAAAISKTAVAPIERVKLLQVHASKQIAADQYKGIIDCYVR 60

Db      61 IPKQGSLSFWRGLNAVIRFEPQALNFARKDKYKQLFLGQVDRHQFWRFFAGNLSAG 120
      61 IPKQGSLSFWRGLNAVIRFEPQALNFARKDKYKQLFLGQVDRHQFWRFFAGNLSAG 120

QY      121 GAAGATSLCEFYPLDFARTRIAAVGR -AOREFHGLDCLTIKTFKSGSLGLVQGFNVS 179
      121 GAAGATSLCEFYPLDFARTRIAAVGRSGTFRERGLDCLVTKTKSGIRGLVQGFNVS 180

Db      121 GAAGATSLCEFYPLDFARTRIAAVGRSGTFRERGLDCLVTKTKSGIRGLVQGFNVS 180

QY      180 VGGIITRAAFEGYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLSLSPDTVRRRRMM 239
      181 VGGIITRAAFYFGYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLSLSPDTVRRRRMM 240

Db      240 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFKFGKAMSNTLRMGGAFAVLVLTDETKKYY 297
      241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFKFGKAMSNTLRMGGAFAVLVLTDETKKYI 298

RESULT 10
US-10-141-478A-2
; Sequence 2, Publication US/10141478A
; Publication No. US20030148300A1
; GENERAL INFORMATION:
; APPLICANT: Valentin, Henry
; APPLICANT: Savage, Thomas
; APPLICANT: Voelker, Toni
; APPLICANT: zang, Wei
; TITLE OF INVENTION: Metabolite Transporters
; FILE REFERENCE: 16515.146

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 19:35:01 ; Search time 20.6204 Seconds

(without alignments)
1385.139 Million cell updates/sec

Title: US-09-811-132-31

Perfect score: 1553

Sequence: 1 MGDHMSFLKDFLAGAVALA.....LRGNGAFVLVDEIKKYV 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1526.5	98.3	298 1	ADP,ATP carrier pr
2	1466.5	94.4	298 1	adenine nucleotide
3	1463.5	94.2	298 1	ADP,ATP carrier pr
4	1458.5	93.9	298 1	ADP,ATP carrier pr
5	1391.5	89.6	298 1	ADP,ATP carrier pr
6	1385.5	89.2	298 1	ADP,ATP carrier pr
7	1380.5	88.9	298 1	ADP,ATP carrier pr
8	1368.5	88.1	298 1	ADP,ATP carrier pr
9	1142.5	73.6	301 1	ADP,ATP carrier pr
10	1045.5	67.3	313 1	ADP,ATP carrier pr
11	1043.5	67.2	313 1	ADP,ATP carrier pr
12	1037.5	66.8	300 2	ADP,ATP carrier pr
13	1005.5	64.7	300 2	ADP,ATP carrier pr
14	973.5	62.7	339 2	ADP,ATP carrier pr
15	904.5	58.2	301 2	ADP,ATP carrier pr
16	772	49.7	306 1	ADP,ATP carrier pr
17	770.5	49.6	308 1	ADP,ATP carrier pr
18	756.5	48.7	387 1	ADP,ATP carrier pr
19	752.5	48.5	322 2	ADP,ATP carrier pr
20	752.5	48.5	386 2	ADP,ATP carrier pr
21	751.5	48.4	387 2	ADP,ATP carrier pr
22	746.5	48.1	379 2	ADP,ATP carrier pr
23	746.5	48.1	382 2	ADP,ATP carrier pr
24	745.5	48.0	326 2	ADP,ATP carrier pr
25	745.5	48.0	386 2	ADP,ATP carrier pr
26	744.5	47.9	386 2	ADP,ATP carrier pr
27	740	47.6	379 2	ADP,ATP carrier pr
28	740	47.6	386 2	ADP,ATP carrier pr
29	737	47.5	385 1	ADP,ATP carrier pr

30	736	47.4	307 2	ADP,ATP carrier pr
31	734	47.3	318 1	ADP,ATP carrier pr
32	733.5	47.2	313 1	ADP,ATP carrier pr
33	729	46.9	305 2	ADP,ATP carrier pr
34	728.5	46.9	306 2	ADP,ATP carrier pr
35	718.5	46.3	309 2	ADP,ATP carrier pr
36	676	43.5	298 2	ADP,ATP carrier pr
37	508	32.7	327 2	ADP,ATP carrier pr
38	368	23.7	415 2	ADP,ATP carrier pr
39	367.5	23.7	325 2	ADP,ATP carrier pr
40	363	23.4	381 2	ADP,ATP carrier pr
41	350.5	22.6	475 2	ADP,ATP carrier pr
42	349.5	22.5	352 2	ADP,ATP carrier pr
43	345.5	22.2	358 2	ADP,ATP carrier pr
44	334.5	21.5	348 2	ADP,ATP carrier pr
45	327	21.1	332 2	ADP,ATP carrier pr

ALIGNMENTS

RESULT 1
AA4778
ADP,ATP carrier protein T1 - human
N:Alternate names: mitochondrial ADP,ATP translocase 1
C:Species: Homo sapiens (man)
C:Date: 17-Mar-2000 #sequence,revision 17-Mar-2000 #text_change 17-Mar-2000
C:Accession: AA4778; S03893; A39891; A28116
R:Li, K.; Warner, C.K.; Hodges, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, J. Biol. Chem. 264, 13998-14004, 1989
A:Title: A human muscle adenine nucleotide translocator gene has four exons, is located
A:Reference number: AA4778; MUID:89340499; PMID:2547778
A:Accession: AA4778
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-298 <LIA>
A:Cross-references: GB:J04982; NID:9178658; PIDN:AAA51736.1; PID:9178659
R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP
A:Reference number: S03893; MUID:8936596; PMID:2541251
A:Accession: S03893
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-298 <COZ>
R:Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A:Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a lea
A:Reference number: A39891; MUID:88041149; PMID:2823266
A:Accession: A39891
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 <NEC>
A:Cross-references: GB:J02966; NID:9339919; PIDN:AAA61223.1; PID:9339920
A:Experimental source: clone PHMAWT
R:Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
A:Reference number: A94197; MUID:86124645; PMID:2829183
A:Accession: A28116
A:Molecule type: mRNA
A:Residues: 1-37 <HOU>
A:Cross-references: GB:J03593; NID:9339724; PIDN:AAA36751.1; PID:9339725
A:Experimental source: liver
A:Gene: GDB:AMT1; T1
A:Cross-references: GDB:119680; OMIM:103220
A:Map position: 4q35-4q35
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrial; transmembrane protein
F:2-398/Product: ADP,ATP carrier protein #status predicted <MAT>
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 98.3%; Score 1526.5; DB 1; Length 298;
Best Local Similarity 98.3%; Pred. No. 1.5e-130;
Matches 293; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 MGDHANSFLKDFLAGVAAVSTKTAAPIERVKLLQVOHASKOISAEKQYKGIIDCVYR 60
|||||
DB 1 MGDHANSFLKDFLAGVAAVSTKTAAPIERVKLLQVOHASKOISAEKQYKGIIDCVYR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDYKQIFLGGVDRHKQFWRFFAGNLAGS 120
|||||
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDYKQIFLGGVDRHKQFWRFFAGNLAGS 120
QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLGDCIIRKFSKDGRLGLYOGFNVS 179
|||||
DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLGDCIIRKFSKDGRLGLYOGFNVS 180
QY 180 VOGIITIRAAVFEVYDTAKGMLDPKKNVHIFVSMIAQSVTAAGLSTPFDVRRRMM 239
|||||
DB 181 VOGIITIRAAVFEVYDTAKGMLDPKKNVHIFVSMIAQSVTAAGLSTPFDVRRRMM 240
QY 240 QSGRKADIMYTGTVDCMRKIANDEGAKAFKGAWSNVLRGMGAFVLYLDEIKRYV 297
|||||
DB 241 QSGRKADIMYTGTVDCMRKIANDEGAKAFKGAWSNVLRGMGAFVLYLDEIKRYV 298

RESULT 2

160173
adenine nucleotide translocator - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999

C:Accession: 160173

R:Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.

Biochim. Biophys. Acta 1152, 192-196, 1993

A:Title: Isolation and characterization of cDNA clones and a genomic clone encoding rat

A:Reference number: 160173; MUID:94002161; PMID:8399300

A:Accession: 160173

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-298 <RES>

A:Cross-references: EMBL:X61667; NID:9400426; PIDN:CAA43842.1; PID:9400427

C:Gene: anti

A:Intons: 37/3; 200/1; 247/1

C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

C:Keywords: duplication; transmembrane protein

F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>

F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 94.4%; Score 1466.5; DB 2; Length 298;

Best Local Similarity 94.3%; Pred. No. 4.1e-125;

Matches 281; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHANSFLKDFLAGVAAVSTKTAAPIERVKLLQVOHASKOISAEKQYKGIIDCVYR 60
|||||
DB 1 MGDHANSFLKDFLAGVAAVSTKTAAPIERVKLLQVOHASKOISAEKQYKGIIDCVYR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDYKQIFLGGVDRHKQFWRFFAGNLAGS 120
|||||
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDYKQIFLGGVDRHKQFWRFFAGNLAGS 120
QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLGDCIIRKFSKDGRLGLYOGFNVS 179
|||||
DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLGDCIIRKFSKDGRLGLYOGFNVS 180
QY 180 VOGIITIRAAVFEVYDTAKGMLDPKKNVHIFVSMIAQSVTAAGLSTPFDVRRRMM 239
|||||
DB 181 VOGIITIRAAVFEVYDTAKGMLDPKKNVHIFVSMIAQSVTAAGLSTPFDVRRRMM 240
QY 240 QSGRKADIMYTGTVDCMRKIANDEGAKAFKGAWSNVLRGMGAFVLYLDEIKRYV 297
|||||

DB 241 QSGRKADIMYTGTVDCMRKIANDEGAKAFKGAWSNVLRGMGAFVLYLDEIKRYV 298

RESULT 3

S37210
ADP, ATP carrier protein T1 - mouse

N:Alternate names: adenine nucleotide carrier

C:Species: Mus musculus (house mouse)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999

C:Accession: S37210

R:Laplace, C.; Costet, P.

submitted to the EMBL Data Library, September 1993

A:Reference number: S37210

A:Accession: S37210

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-298 <IAP>

A:Cross-references: EMBL:X74510; NID:9402627; PIDN:CAA52616.1; PID:9402628

C:Gene: ANCI

C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>

F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1463.5; DB 2; Length 298;

Best Local Similarity 94.0%; Pred. No. 7.6e-125;

Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHANSFLKDFLAGVAAVSTKTAAPIERVKLLQVOHASKOISAEKQYKGIIDCVYR 60
|||||
DB 1 MGDHANSFLKDFLAGVAAVSTKTAAPIERVKLLQVOHASKOISAEKQYKGIIDCVYR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDYKQIFLGGVDRHKQFWRFFAGNLAGS 120
|||||
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDYKQIFLGGVDRHKQFWRFFAGNLAGS 120
QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLGDCIIRKFSKDGRLGLYOGFNVS 179
|||||
DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLGDCIIRKFSKDGRLGLYOGFNVS 180
QY 180 VOGIITIRAAVFEVYDTAKGMLDPKKNVHIFVSMIAQSVTAAGLSTPFDVRRRMM 239
|||||
DB 181 VOGIITIRAAVFEVYDTAKGMLDPKKNVHIFVSMIAQSVTAAGLSTPFDVRRRMM 240
QY 240 QSGRKADIMYTGTVDCMRKIANDEGAKAFKGAWSNVLRGMGAFVLYLDEIKRYV 297
|||||
DB 241 QSGRKADIMYTGTVDCMRKIANDEGAKAFKGAWSNVLRGMGAFVLYLDEIKRYV 298

RESULT 4

XMB0

ADP, ATP carrier protein T1 - bovine

N:Alternate names: ADP/ATP translocase T1

C:Species: Bos primigenius taurus (cattle)

C>Date: 14-Nov-1983 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999

C:Accession: A43646; A24822; A03181; A61343; S69369

R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.

Biochemistry 28, 866-873, 1989

A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently

A:Reference number: A43646; MUID:89229093; PMID:2540808

A:Accession: A43646

A:Molecule type: mRNA

A:Residues: 1-298 <POW>

A:Cross-references: GB:M24102; NID:9529414; PIDN:AAA30768.1; PID:9529415

R:Nasmussen, U.B.; Wohlrab, H.

Biochem. Biophys. Res. Commun. 138, 850-857, 1986

A:Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unus

A:Reference number: A24822; MUID:86295775; PMID:3017341

A:Accession: A24822

A:Molecule type: mRNA

A:Residues: 208-298 <RAS>

A:Cross-references: GB:M13763; NID:g162630; PIDN:AAA30363.1; PID:g162631
 R:Aquila, H.; Mistra, D.; Eulitz, M.; Klingenberg, M.
 Hoppel-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
 A:Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondrion
 A:Reference number: A03181; MUID:82188267; PMID:7076130
 A:Accession: A03181
 A:Molecule type: protein
 A:Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298 <AOU>
 A>Note: residue 52 may be methyllysine
 R:Babel, M.; Wachter, E.; Aquila, H.; Klingenberg, M.
 Biochim. Biophys. Acta 670, 176-180, 1981
 A:Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitochondrion
 A:Reference number: A01343; MUID:82046808; PMID:6271240
 A:Accession: A01343
 A:Molecule type: protein
 A:Residues: 205-298 <DAB>
 R:Oetmeier, W.; Masson, K.; Kalina, S.
 Eur. J. Biochem. 227, 730-733, 1995
 A:Title: ((3)H)-2,4-dichloro-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP/ATP carrier
 A:Reference number: S69369; MUID:95172058; PMID:7867632
 A:Accession: S69369
 A:Molecule type: protein
 A:Residues: 49-63; 154-168 <OET>
 A:Comment: This protein is synthesized in the cytosol and transported into the mitochondrion
 C:Complex: homodimer
 C:Function:
 A:Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP
 A>Note: located in the inner mitochondrial membrane
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mtocch
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>
 F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
 F:52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 93.9%; Score 1458.5; DB 1; Length 298;
 Best Local Similarity 94.3%; Pred. No. 2.2e-124;
 Matches 281; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPLERKLLQVHASKQISAEKQYGIIDCYVR 60
 DB 1 MSDALSLKDFLAGAANAASKTAVAPLERKLLQVHASKQISAEKQYGIIDCYVR 60
 QY 61 IPKEGFLSFMGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKKQFWRFFAGNLSG 120
 DB 61 IPKEGFLSFMGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKKQFWRFFAGNLSG 120
 QY 121 GAAGTSLCFYVPLDFARTRLAADVGR-RAQREFHGLGDCIIRKSDGLKGLYGFNVS 179
 DB 121 GAAGTSLCFYVPLDFARTRLAADVGR-RAQREFHGLGDCIIRKSDGLKGLYGFNVS 179
 QY 180 VOGIIYRAAYFGVDTAKGMLDPKKNVHIFVSMIAQSVTVAGLSTPPTVRRMM 239
 DB 180 VOGIIYRAAYFGVDTAKGMLDPKKNVHIFVSMIAQSVTVAGLSTPPTVRRMM 239
 QY 240 QSGRKADIMYTGTDCKRKIAKDEGAKAFEGGANSNVLRGGAFAVLVLYDEIKKY 297
 DB 240 QSGRKADIMYTGTDCKRKIAKDEGAKAFEGGANSNVLRGGAFAVLVLYDEIKKY 297
 QY 241 QSGRKADIMYTGTDCKRKIAKDEGAKAFEGGANSNVLRGGAFAVLVLYDEIKKY 298
 DB 241 QSGRKADIMYTGTDCKRKIAKDEGAKAFEGGANSNVLRGGAFAVLVLYDEIKKY 298

RESULT 5
 A29132
 ADP/ATP carrier protein T2 - human
 N:Alternate names: mitochondrial ADP/ATP translocase 2
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C:Accession: A29132; C28116
 R:Battini, R.; Ferrarini, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.
 J. Biol. Chem. 262, 4355-4359, 1987
 A:Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulated
 A:Reference number: A29132; MUID:87166056; PMID:3031073
 A:Accession: A29132

A:Molecule type: mRNA
 A:Residues: 1-298 <BAY>
 A:Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247
 R:Houldsworth, J.; Attard, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
 A:Reference number: A94197; MUID:88124845; PMID:2829183
 A:Accession: C28116
 A:Molecule type: mRNA
 A:Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>
 A:Cross-references: GB:J03591; NID:g339720; PIDN:AAA36749.1; PID:g339721
 A:Experimental source: clone PHAT3
 C:Genetics:
 A:Gene: GDB:AMT2; T3; 2F1
 A:Cross-references: GDB:125190; OMIM:300150
 A:Map position: Xq13-qx26
 A>Note: there may be some confusion in the assignment of sequences for GDB:AMT2 and G
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 89.6%; Score 1391.5; DB 1; Length 298;
 Best Local Similarity 88.6%; Pred. No. 2.5e-118;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPLERKLLQVHASKQISAEKQYGIIDCYVR 60
 DB 1 MGDALSLKDFLAGAANAASKTAVAPLERKLLQVHASKQITADQYGIIDCYVR 60
 QY 61 IPKEGFLSFMGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKKQFWRFFAGNLSG 120
 DB 61 IPKEGFLSFMGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKKQFWRFFAGNLSG 120
 QY 121 GAAGTSLCFYVPLDFARTRLAADVGR-RAQREFHGLGDCIIRKSDGLKGLYGFNVS 179
 DB 121 GAAGTSLCFYVPLDFARTRLAADVGR-RAQREFHGLGDCIIRKSDGLKGLYGFNVS 179
 QY 180 VOGIIYRAAYFGVDTAKGMLDPKKNVHIFVSMIAQSVTVAGLSTPPTVRRMM 239
 DB 180 VOGIIYRAAYFGVDTAKGMLDPKKNVHIFVSMIAQSVTVAGLSTPPTVRRMM 239
 QY 240 QSGRKADIMYTGTDCKRKIAKDEGAKAFEGGANSNVLRGGAFAVLVLYDEIKKY 296
 DB 240 QSGRKADIMYTGTDCKRKIAKDEGAKAFEGGANSNVLRGGAFAVLVLYDEIKKY 296
 QY 241 QSGRKADIMYTGTDCKRKIAKDEGAKAFEGGANSNVLRGGAFAVLVLYDEIKKY 297
 DB 241 QSGRKADIMYTGTDCKRKIAKDEGAKAFEGGANSNVLRGGAFAVLVLYDEIKKY 297

RESULT 6
 S03894
 ADP/ATP carrier protein T3 - human
 N:Alternate names: ADP/ATP carrier protein T2 (misidentification); mitochondrial ADP/ATP translocase 2
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C:Accession: S03894; B28116
 R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
 J. Mol. Biol. 206, 261-280, 1989
 A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase
 A:Reference number: S03893; MUID:89336396; PMID:2541251
 A:Accession: S03894
 A>Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-298 <COZ>
 R:Houldsworth, J.; Attard, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
 A:Reference number: A94197; MUID:88124845; PMID:2829183
 A:Accession: B28116
 A:Molecule type: mRNA
 A:Residues: 36-104, 'R', 106, 'A', 109-298 <HOU>
 A:Cross-references: GB:J03592; NID:g339722; PIDN:AAA36750.1; PID:g339723
 A:Experimental source: liver
 C:Genetics:

QY 8 FLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAKOYKGIIDCVIRPKQGF 67
 12 FLIDLSGGTAANAASKTAVAPIERVKLLQVOHASKOISAKOYKGIIDCVIRPKQGF 71
 Db 68 LSFWRGNLANVIRFPTQALNFAFKDKYKQFLGCVDRHKOFRMYFAGNLASGAAGATS 127
 72 AALMRGNLANVIRFPTQALNFAFKDKYKQFLGCVDRHKOFRMYFAGNLASGAAGATS 131
 QY 128 LCFEYVPLDFAFRTLRADAVGRRAQREFHGLDCIIKIFKSDGLNGLYOGFVNSVOGIIYR 187
 132 LCFEYVPLDFAFRTLRADAVGRRAQREFHGLDCIIKIFKSDGLNGLYOGFVNSVOGIIYR 191
 Db 188 AAFEGYVDIAKGM-L-PDPKRVHIFVSMIAQSTAVAGLLSYDPDYRRRMMQSGRKA 246
 192 AAFEGMEDTAKMVFASDQKLNFEFAAGIAQVTVGSGIISYPMDYVRRRMMQSGRK-- 249
 QY 247 DIWYTGVDQMRKIAKDEGAKAFKGMASVNLRGMGAFVLVYDEIKKTV 297
 250 DILKNTLDCAKKTIQNEGMSAFKGLASNVFRTGSLVLAITYDEIQKFL 300

RESULT 13

T15206
 hypothetical protein W02D3.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
 C:Accession: T15206
 R:Le, T.; Weinstein, L.; Rifkin, L.
 submitted to the EMBL Data Library, May 1997
 A:Description: The sequence of C. elegans cosmid W02D3.
 A:Reference number: Z18308
 A:Accession: T15206
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-300 <LEFT>
 A:Cross-references: EMBL:AF003141; NID:g2088732; PID:g2088738; PIDN:AA54179.1; GSPDB:GA
 A:Experimental source: strain Bristol N2; clone W02D3
 C:Gene: CESP:W02D3.6
 A:Map position: 1
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 F:9-103/Domain: ADP,ATP carrier protein repeat homology <ACR>

Query Match 64.7% Score 1005.5; DB 2; Length 300;
 Best Local Similarity 66.0%; Pred. No. 2,2e-83;
 Matches 192; Conservative 40; Mismatches 56; Indels 3; Gaps 2;
 QY 8 FLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAKOYKGIIDCVIRPKQGF 67
 12 FLIDLSGGTAANAASKTAVAPIERVKLLQVOHASKOISAKOYKGIIDCVIRPKQGF 71
 Db 68 LSFWRGNLANVIRFPTQALNFAFKDKYKQFLGCVDRHKOFRMYFAGNLASGAAGATS 127
 72 AAFMRGNLANVIRFPTQALNFAFKDKYKQFLGCVDRHKOFRMYFAGNLASGAAGATS 131
 QY 128 LCFEYVPLDFAFRTLRADAVGRRAQREFHGLDCIIKIFKSDGLNGLYOGFVNSVOGIIYR 187
 132 LCFEYVPLDFAFRTLRADAVGRRAQREFHGLDCIIKIFKSDGLNGLYOGFVNSVOGIIYR 191
 Db 188 AAFEGYVDIAKGM-L-PDPKRVHIFVSMIAQSTAVAGLLSYDPDYRRRMMQSGRKA 246
 192 AAFEGMEDTAKMVFASDQKLNFEFAAGIAQVTVGSGIISYPMDYVRRRMMQSGRK-- 249
 QY 247 DIWYTGVDQMRKIAKDEGAKAFKGMASVNLRGMGAFVLVYDEIKKTV 297
 250 DILKNTLDCAKKTIQNEGMSAFKGLASNVFRTGSLVLAITYDEIQKFL 300

RESULT 14

A41677
 ADP,ATP carrier protein - Chlorella kessleri
 C:Species: Chlorella kessleri
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999

C:Accession: A41677
 R:Halgarth, C.; Sauer, N.; Tanner, W.
 J. Biol. Chem. 266, 24044-24047, 1991
 A:Title: Glucose increases the expression of the ATP/ADP translocator and the glycera
 A:Reference number: A41677; MUID:92084708; PMID:1748677
 A:Accession: A41677
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-339 <HIT>
 A:Cross-references: GB:M76669; NID:g516596; PIDN:AAA33027.1; PID:g516597
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:36-134/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:144-235/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:241-329/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match

Best Local Similarity 62.7%; Score 973.5; DB 2; Length 339;
 Best Local Similarity 65.3%; Pred. No. 2e-80;
 Matches 192; Conservative 30; Mismatches 65; Indels 7; Gaps 4;
 QY 7 SFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEK--OYKGIIDCVIRPK 64
 40 AFYKDLIAGGTAGAIKSTAVAPIERVKLLQVDSNMISGVPRRTGIVNCFVRSSE 99
 Db 65 QGFLSEWRGNLANVIRFPTQALNFAFKDKYKQFLGCVDRHKOFRMYFAGNLASGAAG 124
 100 QGVASEWRGNLANVIRFPTQALNFAFKDKYKQFLGCVDRHKOFRMYFAGNLASGAAG 158
 QY 125 ATSLCFYVPLDFAFRTLRADAVGRRAQREFHGLDCIIKIFKSDGLNGLYOGFVNSVOGII 184
 159 AGSLIYVPLDFAFRTLRADAVGRRAQREFHGLDCIIKIFKSDGLNGLYOGFVNSVOGII 218
 Db 185 IYRAAYEGYVDIAKGM-L-PDPKRVHIFVSMIAQSTAVAGLLSYDPDYRRRMMQSGR 243
 219 VYNGAYVGLDFAKGVLFKDEBRTANFAKAAVAQAVTAGGVLSYDPDYRRRMMQSGR-- 276
 QY 244 KGADIMTGTVDQMRKIAKDEGAKAFKGMASVNLRGMGAFVLVYDEIKKTV 297
 277 -GGEROYNGYTIQDCVRKVAQOEGMKAFKGMASVNLRGMGAFVLVYDEIKKTV 329

RESULT 15

S51132
 ADP,ATP carrier protein - malaria parasite (Plasmodium falciparum)
 N:Alternate names: ADP/ATP transporter
 C:Species: Plasmodium falciparum
 C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jun-2000
 C:Accession: S68993; S51132
 R:Halgin, J.; Jauregui, G.
 Eur. J. Biochem. 228, 86-91, 1995
 A:Title: Molecular characterisation of the ADP/ATP-transporter cDNA from the human m
 A:Reference number: S68993; MUID:95188918; PMID:7883016
 A:Accession: S68993
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-301 <HAT>
 A:Cross-references: EMBL:X83551; NID:g623334; PIDN:CA58541.1; PID:g623335
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:6-103/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:112-203/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:209-301/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 58.2%; Score 904.5; DB 2; Length 301;
 Best Local Similarity 58.3%; Pred. No. 3.1e-74;
 Matches 172; Conservative 48; Mismatches 70; Indels 5; Gaps 4;

QY 7 SFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISA--EKOYKGIIDCVIRPK 64
 8 NFADFLMGISAISKITVTPIERVKMLIQDSDIPEIKSGVETSGIINFKRVSK 67
 Db 65 QGFLSEWRGNLANVIRFPTQALNFAFKDKYKQFLGCVDRHKOFRMYFAGNLASGAAG 124

Db 68 QGVLSIMKGNVANYIRYPTQAFNFAFNDFENIN-PRDQNTDPSKFCVNLISGATAG 126

QY 125 ATSCFCFYPLDPFARTRLADYVGRRAOREPHGLDICIIFKSGDLGELYOGENVSVQGIT 184

Db 127 AISLIYVPLDPFARTRLASLDIGKGRDFOFTGLFDLAKIYKOTGLSTISGFEVSYGIT 186

QY 185 IYRAAYEVYDTAKGML-PDPKNVHILFYSWMLAOSVYANAGLLSTPEDTYVRRMMQSGR 243

Db 187 YKRSYFGLYSAKRLFTNDKNTNIYIKMAVAOSVTLIAGLISYFEDYVRRMMMSGR 246

QY 244 KG-ADIMTGTGDCWRKTAKDEGARAFEPFGAWSNLRKGAFAVLVLYDEIKKYV 297

Db 247 KGRKEIQKKNITDCIKILIRNDEGFEFGFGKAMANYIRKAGGALVLVLYDEIQLKI 301

Search completed: August 28, 2003, 19:43:17
Job time : 21.6204 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 19:28:06 ; Search time 11.9731 Seconds

(without alignments)
1166.524 Million cell updates/sec

Title: US-09-811-132-31

Perfect score: 1533
Sequence: 1 MGDHAWFLKDFLAGAVAA.....LRGNGAFVLYDEIKRYV 297

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	1526.5	98.3	298 1	ADP1_HUMAN P12235 homo sapien
2	1466.5	94.4	298 1	ADP1_RAT P05862 rattus norv
3	1463.5	94.2	298 1	P48962 mus musculu
4	1453.5	93.6	297 1	ADP1_BOVIN P02722 bos taurus
5	1408.5	90.7	298 1	ADP2_MOUSE P51881 mus musculu
6	1407.5	90.6	298 1	ADP2_RAT P09073 rattus norv
7	1398.5	90.1	298 1	ADP2_HUMAN P05441 homo sapien
8	1385.5	88.2	298 1	ADP3_HUMAN P12236 homo sapien
9	1380.5	88.9	298 1	P32007 bos taurus
10	1241	79.9	299 1	ADT_DROME Q26365 drosophila
11	1162.5	74.9	301 1	ADT_ANGA Q27338 anopheles g
12	973.5	63.7	339 1	ADT_CHIKE P31692 chlorella k
13	770.5	49.6	308 1	ADT_CHLRE P27080 chlamydomon
14	756.5	48.7	387 1	ADT1_MAIZE P04709 zea mays (m
15	752.5	48.5	322 1	ADT_SCHPO Q09188 schizosacch
16	752.5	48.5	386 1	ADT1_GOSHI Q23442 gossypium h
17	751.5	48.4	382 1	ADT_ORYSA P16591 oryza sativ
18	751.5	48.4	387 1	P12857 zea mays (m
19	746	48.0	381 1	ADP2_MAIZE P13167 arabidopsis
20	744.5	47.9	386 1	ADP1_SOURU P25083 solanum tub
21	742.5	47.8	331 1	ADP1_WHEAT Q41629 triticum ae
22	740	47.6	386 1	ADP2_SOURU P27081 solanum tub
23	736	47.4	307 1	ADP3_YEAST P18238 saccharomyc
24	734	47.3	318 1	ADP2_YEAST P18239 saccharomyc
25	733.5	47.2	313 1	ADP2_YEAST P02723 neurospora
26	731	47.1	385 1	ADP2_ARATH P40941 arabidopsis
27	729	46.9	305 1	ADT_KULDA P49382 kluyveromyc
28	728.5	46.9	331 1	ADP1_WHEAT Q41630 triticum ae
29	718.5	46.3	309 1	ADP1_YEAST P04710 saccharomyc
30	302.5	19.5	678 1	CMC1_HUMAN O75746 homo sapien
31	300.5	19.3	330 1	GDC_BOVIN O01888 bos taurus
32	296.5	19.1	565 1	CMC3_CAEL O19929 caenorhabdi
33	296.5	19.1	702 1	CMC1_CAEL O21153 caenorhabdi

34	296	19.1	588 1	CMC2_CAEL	Q20799 caenorhabdi
35	295	19.0	322 1	GDC_RAT	P16261 rattus norv
36	292.5	18.8	307 1	ODC2_YEAST	O99297 saccharomyc
37	292	18.8	332 1	GDC_HUMAN	P16260 homo sapien
38	281	18.7	675 1	CMC2_HUMAN	O90150 homo sapien
39	280	18.0	315 1	MFT_HUMAN	O942d1 homo sapien
40	279.5	18.0	676 1	CMC2_MOUSE	O94xx4 mus musculu
41	270.5	17.4	315 1	SA18_HUMAN	O942b2 mus musculu
42	267.5	17.2	325 1	UCP5_MOUSE	O03028 saccharomyc
43	266.5	17.2	310 1	ODC1_YEAST	O95258 homo sapien
44	265.5	17.1	325 1	UCP5_HUMAN	O94v73 drosophila
45	263.5	17.0	695 1	CMC1_DROME	

ALIGNMENTS

RESULT 1	ADP1_HUMAN	STANDARD:	PRT:	298 AA.
ID	ADP1_HUMAN			
AC	P12235:			
DT	01-OCT-1989 (rel. 12, Created)			
DT	01-NOV-1990 (rel. 16, Last sequence update)			
DT	15-SEP-2003 (rel. 42, Last annotation update)			
DE	ADP, ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP			
DE	translocase 1) (Adenine nucleotide translocator 1) (ANT 1).			
GN	SLC25A4 OR ANT1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89236396; PubMed=2541251;			
RA	Cozens A.L., Runswick M.J., Walker J.E.;			
RT	"DNA sequences of two expressed nuclear genes for human mitochondrial			
RT	ADP/ATP translocase.";			
RL	J. Mol. Biol. 206:261-280(1989).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89340499; PubMed=2547778;			
RA	Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.;			
RA	Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;			
RT	"A human muscle adenine nucleotide translocator gene has four exons,			
RT	is located on chromosome 4, and is differentially expressed.";			
RT	J. Biol. Chem. 264:13998-14004(1989).			
RL	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88041149; PubMed=2823266;			
RA	Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;			
RT	"cDNA sequence of a human skeletal muscle ADP/ATP translocator: Jack			
RT	of a leader peptide, divergence from a fibroblast translocator cDNA,			
RT	and coevolution with mitochondrial DNA genes.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).			
RL	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Eye:			
RC	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.C.;			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.;			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.;			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.;			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.;			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.;			
RA	Brownstein M.T., Usdin T.B., Toshiyuki S., Carninci P., Prange C.;			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.;			
RA	Boesk S.A., McWen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.;			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.;			
RA	Villalón D.K., Muzny R.M., Sodergren E.J., Lu X., Gibbs R.A.;			
RA	Fahy J., Helton E., Kertman M., Madan A., Rodrigues S., Sanchez A.;			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.;			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.;			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.;			

RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerich A., Schein J.E., Jones S.J.M., Maria M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RC SEQUENCE OF 1-37 FROM N.A.
 RC TISSUE-Liver;
 RA MEDLINE=88124845; PubMed=2829183;
 RA Houldsworth J., Attardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 RT level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 RN [6]
 RP VARIANTS PEO PRO-114 AND MET-289.
 RA MEDLINE=40385067; PubMed=10926541;
 RA Raukunen J., Juselius J.K., Tirttilä V., Kyttälä A., Zeviani M.,
 RA Comi G.P., Kerenen J., Peltonen L., Sommalainen A.;
 RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance.";
 RL Science 289:782-785(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant
 CC progressive external ophthalmoplegia with various mitochondrial
 CC DNA deletions (PEO). Patients with PEO have mitochondrial
 CC myopathy, progressive external ophthalmoplegia, and other
 CC abnormalities associated with multiple different deletions of
 CC mitochondrial DNA.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC -----
 DR EMBL: J029966; AAA61223.1; -;
 DR EMBL: J035993; AAA36751.1; -;
 DR EMBL: J049982; AAA51736.1; -;
 DR EMBL: BC008664; AAH08664.1; -;
 DR PIR: A44778; A44778.
 DR Genew: HGNC:10990; SLC25A4.
 DR MIM: 103220; -;
 DR MIM: 157640; -;
 DR GO: GO:0005887; C: integral to plasma membrane; TAS.
 DR GO: GO:0005739; C: mitochondrion; TAS.
 DR GO: GO:0015207; F: adenine transporter activity; TAS.
 DR GO: GO:0006091; F: energy pathways; TAS.
 DR GO: GO:0000002; P: mitochondrial genome maintenance; TAS.
 DR GO: GO:0006332; P: small molecule transport; TAS.
 DR InterPro: IPR002067; M1_carrier.
 DR InterPro: IPR002030; M1_uncoupling.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR Pfam: PRO0926; MITOCARRIER.
 DR PRINTS: PRO0784; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family; Disease mutation.
 FT TRANSMEM 13 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.

FT REPEAT 209 298 3.
 FT VARIANT 114 114 A -> P (IN PEO).
 FT VARIANT 289 289 /FTID=VAR_012111.
 FT VARIANT 289 289 V -> M (IN PEO).
 FT VARIANT 289 289 /FTID=VAR_012112.
 FT CONFLICT 16 16 G -> A (IN REF. 3).
 FT CONFLICT 147 149 KGA -> RR (IN REF. 3).
 FT CONFLICT 227 227 V -> L (IN REF. 3).
 SQ SEQUENCE 298 AA; 33064 MW; 59F0DFACAE7CEB8 CRC64;
 Query Match 98.3%; Score 1526.5; DB 1; Length 298;
 Best Local Similarity 98.3%; Pred. No. 2e-129; 2; Indels 1; Gaps 1;
 Matches 293; Conservative 2; Mismatches 2;
 QY 1 MGDHANSFLKDFLAGVAVAASVSTAAPLIERVLLQVQHASQKQSAEKQYKIIDCVAR 60
 DB 1 MGDHANSFLKDFLAGVAVAASVSTAAPLIERVLLQVQHASQKQSAEKQYKIIDCVAR 60
 QY 61 IPEQGFSLFWRGNLANVIRYPTQALNFAFKRYKQLEGVDRKQFWRFRAGNLASG 120
 DB 61 IPEQGFSLFWRGNLANVIRYPTQALNFAFKRYKQLEGVDRKQFWRFRAGNLASG 120
 QY 121 GAAGATSLCFVPLDFAPRLADVGR-RRAQREHGLGDCITIKFRSDGLRGLYOGFPNV 179
 DB 121 GAAGATSLCFVPLDFAPRLADVGR-RRAQREHGLGDCITIKFRSDGLRGLYOGFPNV 180
 QY 180 VQGIITRYRAVFGVYDTAKGMLDPKRNHIFVSMIAQSVTAAGLSYPFDTVRRRMM 239
 DB 181 VQGIITRYRAVFGVYDTAKGMLDPKRNHIFVSMIAQSVTAAGLSYPFDTVRRRMM 240
 QY 240 QSGRKADIMYTGTVDCMKRIADGAKAFKQAMSNVLRGKGAVLYLYDEIKRYV 297
 DB 241 QSGRKADIMYTGTVDCMKRIADGAKAFKQAMSNVLRGKGAVLYLYDEIKRYV 298
 RESULT 2
 ADT1_RAT STANDARD; PRT; 298 AA.
 ID ADT1_RAT
 AC 005962;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
 DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
 GN SLC25A4 OR ANT1.
 OS Rattus norvegicus (Rat).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shiohara Y., Kamida M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 RT encoding rat mitochondrial adenine nucleotide translocator.";
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER
 CC EXTENT, IN BRAIN AND KIDNEY.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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CC EMBL, X61667; CAA43842.1; -
 DR EMBL, D12770; BAA02337.1; -
 DR PIR, I60173; I60173.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 238 AA; 32989 MW; 66704FF78C6BC320 CRC64;

Query Match 94.4%; Score 1466.5; DB 1; Length 298;
 Best Local Similarity 94.3%; Pred. No. 4.7e-124;
 Matches 281; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHAWSLKPLAGAAVAASKTAADIERVKLLQVQVHASKQISAKQYKGIIDCYVR 60
 1 GGDALSLKPLAGAAVAASKTAADIERVKLLQVQVHASKQISAKQYKGIIDCYVR 60
 DB 61 IPKEGFLSPFRGNLANIYRFPYQALNFAFRKDKYKQFLGVDHKGFWYFNGNLASG 120
 61 IPKEGFLSPFRGNLANIYRFPYQALNFAFRKDKYKQFLGVDHKGFWYFNGNLASG 120
 QY 121 GAAGATSLCFYYPPLDFARTLADYGR-RAQREFHGLDCIIFKSGDLNGLYOGFNVS 179
 121 GAAGATSLCFYYPPLDFARTLADYGR-RAQREFHGLDCIIFKSGDLNGLYOGFNVS 179
 DB 121 GAAGATSLCFYYPPLDFARTLADYGR-RAQREFHGLDCIIFKSGDLNGLYOGFNVS 180
 121 GAAGATSLCFYYPPLDFARTLADYGR-RAQREFHGLDCIIFKSGDLNGLYOGFNVS 180
 QY 180 VGGITTYAAAFGYVDYAKGMLPPKKNHIFVSMIAOSVAVAGLSTPPDYVRRMM 239
 180 VGGITTYAAAFGYVDYAKGMLPPKKNHIFVSMIAOSVAVAGLSTPPDYVRRMM 239
 DB 181 VGGITTYAAAFGYVDYAKGMLPPKKNHIFVSMIAOSVAVAGLSTPPDYVRRMM 240
 181 VGGITTYAAAFGYVDYAKGMLPPKKNHIFVSMIAOSVAVAGLSTPPDYVRRMM 240
 QY 240 QSGRKADIMTGTVDCKRKIAKDEGAKAFKGAWSNVLKRGGAFLVLYDEIKKYV 297
 240 QSGRKADIMTGTVDCKRKIAKDEGAKAFKGAWSNVLKRGGAFLVLYDEIKKYV 297
 DB 241 QSGRKADIMTGTVDCKRKIAKDEGAKAFKGAWSNVLKRGGAFLVLYDEIKKYV 298
 241 QSGRKADIMTGTVDCKRKIAKDEGAKAFKGAWSNVLKRGGAFLVLYDEIKKYV 298

RESULT 3
 ADP1_MOUSE STANDARD: PRT: 298 AA.

AC P48962; Q62164; -
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADP_Arp carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (MANT1).
 GN SLC25A4 OR ANT1 OR ANCL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=97059403; PubMed=8903724;
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudoautosomal genes and their mouse homologs.";
 RL Mann. Genome 7:25-30(1996).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Muscle;
 RA Laplace C., Costet P.;
 RL Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes.";
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strassberg R.L., Felting E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Bottingfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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CC EMBL, U27315; AAC52837.1; -
 DR EMBL, X74510; CAA52616.1; -
 DR EMBL, AF240002; AAF64470.1; -
 DR EMBL, BC003791; AAH03791.1; -
 DR EMBL, BC026925; AAH26925.1; -
 DR PIR, S37210; S37210.
 DR MGD; MGI:1353495; SLC25A4.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.

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FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
FT CONFLICT 136 136 F -> L (IN REF. 1).
SQ SEQUENCE 298 AA; 32904 MW; 3A849FEAB0981462 CRC64;

Query Match
Best Local Similarity 94.08; Score 1463.5; DB 1; Length 298;
Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHMSFLDKFLAGAAVAASKTAVAPIERVKLLQVOHASKQISAERKQYGIIDCVVR 60
DB 1 MGDALSLKDELFLAGIAAASKTAVAPIERVKLLQVOHASKQISAERKQYGIIDCVVR 60
QY 61 IPRKQGLSFWKRLANVIRFPQALNFAKDKYKQLFLGCVDRHKOFRYFAGNLSAG 120
DB 61 IPRKQGLSFWKRLANVIRFPQALNFAKDKYKQLFLGCVDRHKOFRYFAGNLSAG 120
QY 121 GAAGATSLCFYPLDFPRTLRADAVGR-RAOREFHGLDCCIIRKFKSDGLRGVYOGFNVS 179
DB 121 GAAGATSLCFYPLDFPRTLRADAVGR-RAOREFHGLDCCIIRKFKSDGLRGVYOGFNVS 180
QY 180 VOGIIIRAAVFGVYDFAKGMPLDPKKNVHIFVSMIAQSVYAVAGLSYEPDVRRRMM 239
DB 181 VOGIIIRAAVFGVYDFAKGMPLDPKKNVHIFVSMIAQSVYAVAGLSYEPDVRRRMM 240
QY 240 QSGRKADIMYTGVDCKRIAKDEGAKAFKGAWSNVLRGSGAFVLYLYDEIKKYV 297
DB 241 QSGRKADIMYTGVDCKRIAKDEGAKAFKGAWSNVLRGSGAFVLYLYDEIKKYV 298

RESULT 4
ADT1_BOVIN STANDARD; PRT; 297 AA.
AC P02722;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP,ATP carrier protein, heart isoform T1 (ADP/ATP translocase 1)
DE (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-89229093; PubMed-2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues.";
RL Biochemistry 28:866-873(1989).
RN [2]
RP SEQUENCE.
RX MEDLINE-82188267; PubMed-7076130;
RA Aquila H., Mista D., Eulitz M., Klingenberg M.;
RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
RT mitochondria.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).
RN [3]
RP SEQUENCE OF 207-297 FROM N.A.
RX MEDLINE-86295775; PubMed-3017341;
RA Rasmussen U.B., Wohlb H.;
RT Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and
RT an unusually short 3'-noncoding sequence.";
RL Biochem. Biophys. Res. Commun. 138:850-857(1986).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

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CC or send an email to license@isb.slb.ch).
CC -----
DR EMBL: M13783; AAA30363.1; -.
DR EMBL: M24102; AAA30768.1; -.
DR PIR: A43646; XERO.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR002030; Mlt_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mlt_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family; Methylation.
FT MOD_RES 1 1 BLOCKED.
FT INT_MET 0 0 METHYLATION (POTENTIAL).
FT TRANSRES 51 51 1 (POTENTIAL).
FT TRANSRES 11 28 2 (POTENTIAL).
FT TRANSRES 72 90 3 (POTENTIAL).
FT TRANSRES 116 133 4 (POTENTIAL).
FT TRANSRES 175 194 5 (POTENTIAL).
FT TRANSRES 213 230 6 (POTENTIAL).
FT TRANSRES 272 290 1 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 207 2.
FT REPEAT 208 297 3.
SQ SEQUENCE 297 AA; 32836 MW; A582D3C4A40AE848 CRC64;

Query Match
Best Local Similarity 93.64; Score 1453.5; DB 1; Length 297;
Matches 280; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

QY 3 DHAMSFLLDKFLAGAAVAASKTAVAPIERVKLLQVOHASKQISAERKQYGIIDCVVRIP 62
DB 2 DQALSLKDELFLAGIAAASKTAVAPIERVKLLQVOHASKQISAERKQYGIIDCVVRIP 61
QY 63 KEQGLSFWKRLANVIRFPQALNFAKDKYKQLFLGCVDRHKOFRYFAGNLSAG 122
DB 62 KEQGLSFWKRLANVIRFPQALNFAKDKYKQLFLGCVDRHKOFRYFAGNLSAG 121
QY 123 AGATSLCFYPLDFPRTLRADAVGR-RAOREFHGLDCCIIRKFKSDGLRGVYOGFNVSQ 181
DB 122 AGATSLCFYPLDFPRTLRADAVGR-RAOREFHGLDCCIIRKFKSDGLRGVYOGFNVSQ 181
QY 182 GIITIRAAVFGVYDFAKGMPLDPKKNVHIFVSMIAQSVYAVAGLSYEPDVRRRMMOS 241
DB 182 GIITIRAAVFGVYDFAKGMPLDPKKNVHIFVSMIAQSVYAVAGLSYEPDVRRRMMOS 241
QY 242 GRRKADIMYTGVDCKRIAKDEGAKAFKGAWSNVLRGSGAFVLYLYDEIKKYV 297
DB 242 GRRKADIMYTGVDCKRIAKDEGAKAFKGAWSNVLRGSGAFVLYLYDEIKKYV 297

RESULT 5
ADT2_MOUSE STANDARD; PRT; 298 AA.
AC P51881; Q61311;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP,ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.

```

OX NCB1_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=97059403; PubMed=8903724;
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudautosomal genes and their mouse
 homologs.";
 RL Mamm. Genome 7:25-30(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA Sheldon J.G.;
 RL Thesis (1995), University of Cambridge, U.K.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RA Coster P., Laplace C.;
 RL Submitted (FEB-1993) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP REVISIONS.
 RA Laplace C.;
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20432087; PubMed=10974536;
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide
 translocase 1 and 2 genes.";
 RL Gene 254:57-66(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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 CC -----
 DR EMBL: U27316; AAC52838.1; -
 DR EMBL: U10404; AAI19009.1; -
 DR EMBL: X70847; CAA50196.1; -
 DR EMBL: AF240003; AAF64471.1; -
 DR MGI: 1353496; SLC25a5.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR002030; Mitoch_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32931 MW; 0798E04B987FE20 CRC64;
 Query Match 90.7%; Score 1408.5; DB 1; Length 298;
 Best Local Similarity 89.6%; Pred. No. 7,3e-119;

Matches 266; Conservative 17; Mismatches 13; Indels 1; Gaps 1;
 QY 1 MGDHWSFLKDLFAGAAVAASKTAVAPLERKYLQVQASKOISAEKQYGIIDCVRR 60
 DB 1 MTDAVSAFKDLFAGVAAIAISKTNAPIERKLLQVQASKOISAEKQYGIIDCVRR 60
 QY 61 IPKEGGLFSFWRGNLANVIRYPTQALNFAFDKTKQLFLGVDRKQWRFPAGLASC 120
 DB 61 IPKEGGLFSFWRGNLANVIRYPTQALNFAFDKTKQLFLGVDRKQWRFPAGLASC 120
 QY 121 GAAGATSLCEVYPLDPAFTRILADVGR--AOREFHGIGCIIFKIFSDGLGYGFENVS 179
 DB 121 GAAGATSLCEVYPLDPAFTRILADVGR--AOREFHGIGCIIFKIFSDGLGYGFENVS 180
 QY 180 VGGIITRYAAYGVYDTAKGMLPDPKAVHIFVSMIAQSVTAAGLSYFPDTRRRAM 239
 DB 181 VGGIITRYAAYGVYDTAKGMLPDPKAVHIFVSMIAQSVTAAGLSYFPDTRRRAM 240
 QY 240 OSGRKADIMYGTVDGCKRIAKDEGAKAFPKGAMSNVLKMGCAFVLVLYDEIKKY 296
 DB 241 OSGRKGTDMYGTGLDCWRKRIADEGSKAFKGMNSNVLKMGCAFVLVLYDEIKKY 297
 RESULT 6
 ADT2_RAT STANDARD; PRT; 298 AA.
 ID ADT2_RAT
 AC 009073;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 DE (Adenine nucleotide translocator 2) (ANT 2).
 GN SLC25A5 OR ANT2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCB1_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shiohara Y., Kamada M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 RT encoding rat mitochondrial adenine nucleotide translocator.";
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
 CC SKELETAL MUSCLE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D12771; BAA02338.1; -
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR002030; Mlt_uncoupling.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.

```

FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32901 MW; 6A59204B987EEF35 CRC64;

Query Match 90.6%; Score 1407.5; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 9e-119;
Matches 266; Conservative 16; Mismatches 14; Indels 1; Gaps 1;

OY 1 MGDHANSFLKDFLAGAANAASKTAVAPIERVKLLLOVHASQISAQKQYKGIIDCVR 60
DB 1 MTDAAVSFAKDFLAGGAAIAISKTAVAPIERVKLLLOVHASQITADKQYKGIIDCVR 60
OY 61 IPKQGLSFWRCNLAVIRYPTQALNFAFKDKYKQLFGVDNRHKQFRRYFAGNLASG 120
DB 61 IPKQGLSFWRCNLAVIRYPTQALNFAFKDKYKQLFGVDNRHKQFRRYFAGNLASG 120
OY 121 GAAGATSLCEVYPLDFARTLADYGR-AOREFHGLDCITIKFKSDGLRGLYQGFNVS 179
DB 121 GAAGATSLCEVYPLDFARTLADYGR-AOREFHGLDCITIKFKSDGLRGLYQGFNVS 180
OY 180 VOGIIIRAYAFGVYDTAKGMLPDPKRVHIFVSMINOSYAVAGLSYFPDVRRRMM 239
DB 181 VOGIIIRAYAFGVYDTAKGMLPDPKRVHIFVSMINOSYAVAGLSYFPDVRRRMM 240
OY 240 QSGRKGADIMYGTGTCWDRKRIADDEGAKAEFFKAGMSVNLGKGAFVLYLDEIKKY 296
DB 241 QSGRKGADIMYGTGTCWDRKRIADDEGAKAEFFKAGMSVNLGKGAFVLYLDEIKKY 297

RESULT 7
ADT2_HUMAN STANDARD; PRT; 298 AA.
ID ADT2_HUMAN
AC P05141; O43350;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP, ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
GN (Adenine nucleotide translocator 2) (ANT 2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90375457; PubMed=2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wurtzel J.;
RT "The human fibroblast adenine nucleotide translocator gene. Molecular
RT cloning and sequence."
RL J. Biol. Chem. 265:16060-16063(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87160056; PubMed=3031073;
RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
RA Baserga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
RT growth-regulated."
RL J. Biol. Chem. 262:4355-4358(1987).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen C.N., Su Y., Baydayan P., Siruno A., Nagaraja R.,
RA Mazzerella R.A., Schlusser D., Chen E.Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.

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RA Becker M., Graves T., Ozersky P.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Altardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC
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CC -----
DR EMBL: M57424; AAA51737.1; -
DR EMBL: J02683; AAA35579.1; -
DR EMBL: L78810; AAB39266.1; -
DR EMBL: AC004000; AAB96347.1; -
DR EMBL: J03591; AAA36749.1; -
DR PIR: A29132; A29132.
DR Genew: HGNC:10991; SLC25A5.
DR MIM: 300150; -
DR GO: GO:0005867; C: Integral to plasma membrane; TAS.
DR GO: GO:0015287; F: adenine transporter activity; TAS.
DR GO: GO:0006832; P: small molecule transport; TAS.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR002030; Mlt_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mltc_carri; 3.
DR PRINTS: PRO00926; MITOCARRIER.
DR PRINTS: PRO0784; MTNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
FT CONFLICT 6 6 V -> L (IN REF. 2).
FT CONFLICT 66 66 G -> E (IN REF. 2).
FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
FT CONFLICT 162 162 V -> G (IN REF. 5).
SQ SEQUENCE 298 AA; 32895 MW; F973C3AED92C49D3 CRC64;

Query Match 90.1%; Score 1398.5; DB 1; Length 298;
Best Local Similarity 88.9%; Pred. No. 8.5e-118;
Matches 264; Conservative 17; Mismatches 15; Indels 1; Gaps 1;

OY 1 MGDHANSFLKDFLAGAANAASKTAVAPIERVKLLLOVHASQISAQKQYKGIIDCVR 60
DB 1 MTDAAVSFAKDFLAGGAAIAISKTAVAPIERVKLLLOVHASQITADKQYKGIIDCVR 60
OY 61 IPKQGLSFWRCNLAVIRYPTQALNFAFKDKYKQLFGVDNRHKQFRRYFAGNLASG 120
DB 61 IPKQGLSFWRCNLAVIRYPTQALNFAFKDKYKQLFGVDNRHKQFRRYFAGNLASG 120

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OY 121 GAAATSTLCFYPPDPFARTRLAADYGR-AOREFHGLDCLIKIFKSDGLNGLYOGENVS 179
DB 121 GAAATSTLCFYPPDPFARTRLAADYGR-AOREFHGLDCLIKIFKSDGLNGLYOGENVS 180
OY 180 VOGIIITRAAYEGYVDYAKGMLPDPKNVHIFVSMIAOSVTAAGLSYPPDYARRMM 239
DB 181 VOGIIITRAAYEGYVDYAKGMLPDPKNVHIFVSMIAOSVTAAGLSYPPDYARRMM 240
OY 240 OSGRRGADIMYTGTVDCWRKIKAKDEGAKAFKGAWSNVLKMGAFVLYLDEIKKY 296
DB 241 OSGRRGADIMYTGTVDCWRKIKAKDEGAKAFKGAWSNVLKMGAFVLYLDEIKKY 297

RESULT 8
ADT3_HUMAN STANDARD; PRT; 298 AA.
ID ADT3_HUMAN
AC P12236; Q96C49;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)
DE (Adenine nucleotide translocator 3) (ANT 3).
GN SLC25A6 OR ANT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:89236396; PubMed-2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
RL J. Mol. Biol. 206:261-280(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain, Cervix, Eye, and lung;
RX MEDLINE:22388257; PubMed-12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schenker C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore J., Max S.I., Wang J., Hsieh F.,
RA Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriques S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 36-298 FROM N.A.
RC TISSUE-Liver;
RX MEDLINE:86124845; PubMed-2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.

```

```

CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
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CC -----
DR EMBL, J03592; AAA6750.1; -
DR EMBL, AY007135; AAG01998.1; -
DR EMBL, BC007295; AAH07295.1; -
DR EMBL, BC007850; AAH07850.1; -
DR EMBL, BC008737; AAH08737.1; -
DR EMBL, BC008935; AAH08935.1; -
DR EMBL, BC014775; AAH14775.1; -
DR PIR, S03894; S03894.
DR Genew: HGNC:10992; SLC25A6.
DR MIM, 300151; -
DR GO, GO:0005744; C:mitochondrial inner membrane translocase co. .; TAS.
DR GO, GO:0005471; F:ATP/ADP antiporter activity; NAS.
DR GO, GO:0006854; P:ATP/ADP exchange; TAS.
DR InterPro, IPR002067; Mtc_carrier.
DR InterPro, IPR002030; Mtc_uncoupling.
DR InterPro, IPR001993; Mito_carr_3.
DR Pfam, PF00153; mito_carr_3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE, PS00784; MITOCARRIER.
DR PROSITE, PS00215; MITOCH_CARRIER.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 231 291 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 100 1.
FT REPEAT 101 208 2.
FT REPEAT 209 298 3.
FT REPEAT 105 108 3.
FT REPEAT 242 242 S -> F (IN REF. 3; AAH14775).
FT CONFLICT 105 108 KHTQ -> RHA (IN REF. 4).
FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).
SQ SEQUENCE 298 AA; 32866 MW; 18534E9F0E49672F CRC64;

Query Match 89.2%; Score 1385.5; DB 1; Length 298;
Best Local Similarity 87.2%; Pred. No. 8.4e-117;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
OY 1 MGDHMSFLKDLFLAGAAVAASVKTAVPIERVKLLQVOHASKOISAEKQYGIIDCYVR 60
DB 1 MTEQAISFKDPLAGIAAIAKSTAVPIERVKLLQVOHASKOIAADKQYGYIDCYVR 60
OY 61 IPKEGFLSTFWGNLANVIRYPTQALNFAFDKTKQLFLGVDYDRKQWRFPAGNLASG 120
DB 61 IPKEGFLSTFWGNLANVIRYPTQALNFAFDKTKQLFLGVDYDRKQWRFPAGNLASG 120
OY 61 IPKEGVLSFWGNLANVIRYPTQALNFAFDKTKQLFLGVDYDRKQWRFPAGNLASG 120
DB 61 IPKEGVLSFWGNLANVIRYPTQALNFAFDKTKQLFLGVDYDRKQWRFPAGNLASG 120
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DB 121 GAAATSTLCFYPPDPFARTRLAADYGR-AOREFHGLDCLIKIFKSDGLNGLYOGENVS 180
OY 180 VOGIIITRAAYEGYVDYAKGMLPDPKNVHIFVSMIAOSVTAAGLSYPPDYARRMM 239
DB 181 VOGIIITRAAYEGYVDYAKGMLPDPKNVHIFVSMIAOSVTAAGLSYPPDYARRMM 240
OY 240 OSGRRGADIMYTGTVDCWRKIKAKDEGAKAFKGAWSNVLKMGAFVLYLDEIKKY 297
DB 241 OSGRRGADIMYTGTVDCWRKIKAKDEGAKAFKGAWSNVLKMGAFVLYLDEIKKY 298

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RESULT 9
ADT3_BOVIN STANDARD; PRT; 298 AA.
AC P32007;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, isoform T2 (ADP/ATP translocase 3) (adenine
nucleotide translocator 3) (ANT 3).
GN SLC25A6 OR ANT3
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89229093; PubMed=2540808;
RT Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
differences in various tissues.";
RT Biochemistry 28:866-873(1989).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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CC or send an email to license@isb-sib.ch).
DR EMBL: M24103; AAA30769.1; -
DR PIR: B43646; B43646.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR002030; Mlt_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 2 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32877 MW; 1C34E7DF6EDE4061 CRC64;

Query Match 88.9%; Score 1380.5; DB 1; Length 298;
Best local Similarity 86.9%; Pred. No. 2,4e-116;
Matches 259; Conservative 21; Mismatches 17; Indels 1; Gaps 1;
OY 1 MGDHMSFKDFLAGVANAANKSTAPLIERVKLLQVGHASQISAEQYKGIIDCVAR 60
DB 1 MTEQALISFKADFLAGGIAAISTAAPIERVKLLQVGHASQIADQYKGIIDCVAR 60
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DB 61 IRKEQGLSFWKGNLANVIRYPTQALNFAKDKYKQLFGVGRHKOFRYRYPAGMLASG 120

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OY 121 GAAGATSLCFVYLPDPAFRLADAVGR- AQREFHGLGDCIIRKFSKSGRLGYGFNVS 179
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DB 181 VGGIIIRAAVFCVYDTAKMLDPKKNHIFVSMIAQSVTAVALISYFDTVRRMM 240
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RESULT 10
ADT_DROME STANDARD; PRT; 299 AA.
AC Q26365; P91614; Q26254; Q95830; Q9VZ70;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP/ATP carrier protein (ADP/ATP translocase) (adenine nucleotide
translocator) (ANT) (stress sensitive B protein).
GN SSB OR A/A-T OR C616944.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92389367; PubMed=1387687;
RT Louvi A., Tellion S.G.;
RT "A cDNA clone encoding the ADP/ATP translocase of Drosophila
RT melanogaster shows a high degree of similarity with the mammalian
RT ADP/ATP translocases";
RT J. Mol. Evol. 35:44-50(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350065; PubMed=7520869;
RT Hutter P., Karch F.;
RT "Molecular analysis of a candidate gene for the reproductive
RT isolation between sibling species of Drosophila.";
RT Experientia 50:749-762(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-Oregon-R.
RA Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburner M.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
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 RA Svirskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Wolley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*";
 RL Science 287:2185-2195(2000).
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN-Berkeley; TISSUE-Larva, Ovary, and Pupa;
 RA MEDLINE-22426066; PubMed-12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champagne M.,
 RA George R.A., Guarin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celniker S.E.;
 RT "A *Drosophila* full-length cDNA resource";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 CC -1- FUNCTION: Catalyzes the exchange of ADP and ATP across the
 CC mitochondrial inner membrane.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).
 CC -1- DOMAIN: Composed of three homologous domains.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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 DR EMBL: S43651; AAB23114.1; -
 DR EMBL: S71762; AAB31734.3; -
 DR EMBL: Y10618; CAA71628.1; -
 DR EMBL: AE003484; AAF47957.1; -
 DR EMBL: AY060978; AAL28526.1; -
 DR EMBL: AY070894; AAL48516.1; -
 DR FLYbase: FBgn0003360; seqB.
 DR GO: GO:0005743; C:mitochondrial inner membrane; IEP.
 DR GO: GO:0006839; P:mitochondrial transport; IMP.
 DR InterPro: IPR002067; Mtl_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 2.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport.
 KW Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport.
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 FT TRANSMEM 34756 34774
 FT TRANSMEM 34840 34858
 FT TRANSMEM 34924 34942
 FT TRANSMEM 35008 35026
 FT TRANSMEM 35092 35110
 FT TRANSMEM 35176 35194
 FT TRANSMEM 35260 35278
 FT TRANSMEM 35344 35362
 FT TRANSMEM 35428 35446
 FT TRANSMEM 35512 35530
 FT TRANSMEM 35596 35614
 FT TRANSMEM 35680 35698
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 FT TRANSMEM 35848 35866
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 FT TRANSMEM 36016 36034
 FT TRANSMEM 36100 36118
 FT TRANSMEM 36184 36202
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 FT TRANSMEM 36352 36370
 FT TRANSMEM 36436 36454
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 FT TRANSMEM 40888 40906
 FT TRANSMEM 40972 40990
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 FT TRANSMEM 41140 41158
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 FT TRANSMEM 45680 45698
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 FT TRANSMEM 46184 46


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DR PIR, S30259, S30259, Mit_carrier.
DR InterPro: IPR002067; Mitochondrial_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 74 92 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 178 197 4 (POTENTIAL).
FT TRANSMEM 217 234 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
SQ SEQUENCE 308 AA; 33528 MW; D477CF0E2B7A53F CRC64;

Query Match
Best Local Similarity 52.6%; Score 770.5; DB 1; Length 308;
Matches 159; Conservative 49; Mismatches 17; Gaps 6;

QY 7 SFLKDELGAGVAANAASKTAVAPIERVKLLIQVO-HASKQISAEKQYGIIDCVVRIPKEQ 65
DB 7 NFMVDELGAGLSAAVSKTAAPIERVKLLIQNDDEMIKGRSLASPYKGIQECFRTVREE 66
QY 66 GELSTFRGNLANVIRFPTQALNFAFKDKYKQLFLGVDNRHKOFWRFPAGNLASGAGA 125
DB 67 GGSLSMRGNTANVIRFPTQALNFAFKDKERMF--GFNKKDEYKWFAGNMAASGAGA 124
QY 126 TSLCFEYPLDFAFTRLAADVGR---AOREFHGLGDCIIRKSPDGLGYGFNVYQ 181
DB 125 VLSLFEYSLDYARTRLANDAKSKKGGROFNGLDVYRKTIASGICGLIKHGFNTSCV 184
QY 182 GIIIRAAVEGYVDYTAGK-MLPDPKNVHIFVSMIAQSVAVAGLLSTPEDEVRRRMQ 240
DB 185 GIIVYRGILFGMDISLKPVLVGLPPLANNFLAFLGMITIGGLASYPIDTIRRRMM 244
QY 241 SGRKGDIMVTGIVDCMKRIADDEGAKAFKFGMSVNLKMGCAFVLVYDEL-----K 294
DB 245 S---GSAVRYNSSEHFCOEIVNKGMSLFGAGANILRAVAGAVLAGYDQIQLVLLK 301
QY 295 KY 296
DB 302 KY 303

RESULT 14
ADP1_MAIZE STANDARD; PRT; 387 AA.
AC ADP1_MAIZE
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP, ATP carrier protein 1, mitochondrial precursor (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
GN ANTI OR ANT-G1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MUTIND-ER7205034;
RX MEDLINE=91322533; PubMed=1863785;
RA Wlansing B.M., Day C.D., Sarah C.J., Leaver C.J.;
RT Nucleotide sequence of two cDNAs encoding the adenine nucleotide translocator from Zea mays L.;
RL Plant Mol. Biol. 17:305-307(1991).
RN [2]
RP SEQUENCE OF 59-387 FROM N.A.
RC STRAIN=CV, B37N;
RX MEDLINE=89338399; PubMed=2547608;
RA Leaver C.J., Bathgate B., Baker A.;
RT Two genes encode the adenine nucleotide translocator of maize

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RT mitochondria. Isolation, characterisation and expression of the
RT structural genes."
RL Eur. J. Biochem. 183:303-310(1989).
RN [3]
RP SEQUENCE OF 70-387 FROM N.A.
RX MEDLINE=85297781; PubMed=2994015;
RA Baker A., Leaver C.J.;
RT Isolation and sequence analysis of a cDNA encoding the ATP/ADP translocator of Zea mays L."
RL Nucleic Acids Res. 13:5857-5867(1985).
CC -!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
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CC -----
DR EMBL: X57556; CAA40781.1; -
DR EMBL: X15711; CAA3742.1; -
DR EMBL: X02842; CAA26600.1; -
DR PIR: S14876; S14876.
DR MAZEDB: 17145; -
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR001993; Mitochondrial_carrier.
DR Pfam: PF00153; mito_carr; 3
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Transil peptide; Multigene family.
FT TRANSLIT 1 77 MITOCHONDRION.
FT CHAIN 78 387 ADP-ATP CARRIER PROTEIN 1.
FT TRANSMEM 91 108 1 (POTENTIAL).
FT TRANSMEM 153 171 2 (POTENTIAL).
FT TRANSMEM 196 213 3 (POTENTIAL).
FT TRANSMEM 257 276 4 (POTENTIAL).
FT TRANSMEM 296 313 5 (POTENTIAL).
FT TRANSMEM 352 370 6 (POTENTIAL).
FT CONFLICT 102 102 K -> E (IN REF. 2).
FT CONFLICT 154 154 N -> Y (IN REF. 3).
SQ SEQUENCE 387 AA; 42391 MW; DE73BB0F478BD57D CRC64;

Query Match
Best Local Similarity 48.7%; Score 756.5; DB 1; Length 387;
Matches 164; Conservative 41; Mismatches 77; Indels 23; Gaps 7;

QY 7 SFLKDELGAGVAANAASKTAVAPIERVKLLIQVO-HASKQISAEKQYGIIDCVVRIPKEQ 65
DB 86 NFMVDELGAGLSAAVSKTAAPIERVKLLIQNDDEMIKGRSLASPYKGIQECFRTIKDE 145
QY 66 GELSTFRGNLANVIRFPTQALNFAFKDKYKQLFLGVDNRHKOFWRFPAGNLASGAGA 125
DB 146 GGSLSMRGNTANVIRFPTQALNFAFKDKERMF--GFNKKDEYKWFAGNMAASGAGA 204
QY 126 TSLCFEYPLDFAFTRLAADVGR---AOREFHGLGDCIIRKSPDGLGYGFNVYQ 182
DB 205 SLSLFEYSLDYARTRLANDAKKAGGGERFNGLDVYRKTLSAGIAGLHGFNTSCVG 264
QY 183 IIRYRAVEGYVDYTAGK---GMIPDPKNVHIFVSMIAQSVAVAGLLSTPEDEVRRRM 237
DB 265 IIVYRGILFGYDSIRPVLTGMLQD---NFPASFLGLMLTNGAGLASYPIDTVRRM 320
QY 238 MMSGRKGDIMVTGIVDCMKRIADDEGAKAFKFGMSVNLKMGCAFVLVYDEL----- 293
DB 321 MMSGGA---VKYKSSIDARQIILKKEGPKSLFGAGANILRAVAGAVLAGYDQIQLV 377

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OY 294 --KRY 296
 DB 378 FGKRY 382
 RESULT 15
 ADP_SCHPO STANDARD; PRT; 322 AA.
 ID ADP_SCHPO
 AC 009188;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADP, ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
 translocator) (ANT).
 GN ANCI OR SPBC530.10C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 NX NCBI_TaxID=4896;
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=96257204; PubMed=8675018;
 RA Couzin N., Trezeguet V., Saux A.L., Lauguin G.J.M.;
 RT "Cloning of the gene encoding the mitochondrial adenine nucleotide
 carrier of Schizosaccharomyces pombe by functional complementation in
 RT Saccharomyces cerevisiae.";
 RL Gene 171:113-117(1996).
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=31848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Soudos V., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Oliver P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Rotherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skellon J., Simmonds M., Squares R., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Voicikert G., Aert R., Robben J., Grymoprez B.,
 RA Wellens J., Vansteede E., Rieger M., Scheffer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leinach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Leleau V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Rhode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RT Nature 415:871-880(2002).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Z49974; CA90275.1; -
 DR EMBL; AL023634; CAA19176.1; -
 DR PIR; T40526; T40526
 DR GenedB_Spomb; SPBC530.10C; -
 DR InterPro; IPR002067; Mlt_carrier.
 DR Pfam; PF00153; mltc_carri; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 2.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 28 48 1 (POTENTIAL).
 FT TRANSMEM 93 111 2 (POTENTIAL).
 FT TRANSMEM 131 151 3 (POTENTIAL).
 FT TRANSMEM 197 217 4 (POTENTIAL).
 FT TRANSMEM 222 242 5 (POTENTIAL).
 FT TRANSMEM 289 309 6 (POTENTIAL).
 SQ SEQUENCE 322 AA; 35020 MW; 8AC3D16A0F41AFC CRC64;
 Query Match 48.5%; Score 752.5; DB 1; Length 322;
 Best Local Similarity 52.9%; Pred. No. 4,4e-60;
 Matches 156; Conservative 51; Mismatches 75; Indels 13; Gaps 6;
 OY 7 SFLKDLGAVAAVSTAVAPIERVKLLQVHASQISAER--QYGIIDCVVRIPK 63
 DB 26 TFFDFPMGVSAVASTAAPIERVKLLIQN--DEMIRAGRLSHRYKGIGCEFKRTAA 83
 OY 64 EGGFLSTFRGLAVIVYFPQALNFAFKKRYKOLFGLGVDNRHGFRRYFNGNLASGAA 123
 DB 84 EEGVLSLRGNTAVLRFPQALNFAFKKRYKOLFGLGVDNRHGFRRYFNGNLASGAA 142
 OY 124 GATSLCEVYPLDFAFRTLAAD--VGRRAQHEFGIGDCIIRKPSDGLRGLYOGFNVSV 180
 DB 143 GAALLLVYSLDYARTLANDAKSAKGGEGFGLVDYRTKTRSGRLGTYGFGPSV 202
 OY 181 QGIITRAAYFGVYDTAKG-MLPDPKNVHIFVSMIAOSTAVAGLLSTPEPTVRRRMM 239
 DB 203 VGIYVYRGIVFGMDTLKPVLYVPLGNGFLASPLGMAVYTGSGVASYPLDTIRRRMM 262
 OY 240 QSGKRGADIMYTGVDCKRKARKDEGAKAFKFGKMSVNLGNGAFVLYLXDEK 294
 DB 263 TSGEA--VYSSFECEGRQLAEGARSPFGKAGANILRGVAGVLYSTDOVO 314

Search completed: August 28, 2003, 19:39:30
 Job time : 12.9731 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 19:34:36 ; Search time 50.2206 Seconds
(without alignments)
1526.099 Million cell updates/sec

Title: US-09-811-132-31

Perfect score: 1553
Sequence: 1 MGDHMSFLKDFLAGAFAA.....LRGNGAFVLVDEIKKYV 297

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1464.5	94.3	298	6	O46373 oryctolagus
2	1462.5	94.2	298	11	Q8BV19 Q8BV19 mus musculus
3	1411.5	90.9	298	6	O8SQH5 Q8SQH5 bos taurus
4	1392.5	89.7	298	13	O8AYM3 O8AYM3 gallus galli
5	1377.5	88.7	298	13	O9YIC4 O9YIC4 rana rugosa
6	1377.5	88.7	298	13	O9PRH1 O9PRH1 rana rugosa
7	1375.5	88.6	298	13	O8JHT0 O8JHT0 brachydontio
8	1374.5	88.5	298	13	O9PRH2 O9PRH2 rana rugosa
9	1366.5	88.0	298	13	O919M9 O919M9 xenopus lae
10	1245.5	80.2	299	5	O95VX4 O95VX4 ethiostigm
11	1241.5	79.9	300	5	O9NHWS O9NHWS lucilia cup
12	1241	79.9	312	5	O8IRAO O8IRAO drosophila
13	1234.5	79.5	317	13	O91336 O91336 rana sylvat
14	1183	76.2	288	5	O44094 O44094 drosophila
15	1183	76.2	288	5	O44093 O44093 drosophila
16	1180.5	76.0	254	11	Q8BK05 Q8BK05 mus musculus

17	1147	73.9	307	5	O62526 O62526 drosophila
18	1139.5	73.4	304	5	O25129 O25129 halocynthia
19	1101.5	70.9	315	4	O9H0C2 O9H0C2 homo sapien
20	1045.5	67.3	313	5	P91410 P91410 caenorhabd
21	1043.5	67.2	313	5	O21103 O21103 caenorhabd
22	1042	67.1	310	10	O8H727 O8H727 phytophor
23	1037.5	66.8	300	5	O45865 O45865 caenorhabd
24	1005.5	64.7	300	5	O01813 O01813 caenorhabd
25	993.5	64.0	300	5	O17407 O17407 caenorhabd
26	989.5	63.7	309	5	O97470 O97470 dicyostell
27	959	61.8	307	8	O9XM22 O9XM22 ascaris suu
28	950	61.2	318	5	O9BJ36 O9BJ36 toxoplasma
29	926.5	59.7	301	5	O8WVR4 O8WVR4 euploies sp
30	916.5	59.0	308	5	O8WVR8 O8WVR8 nyctotherus
31	914.5	58.9	305	5	O8WVR7 O8WVR7 nyctotherus
32	913.5	58.8	306	5	O8WVR5 O8WVR5 nyctotherus
33	908.5	58.5	301	5	O81J34 O81J34 plasmodium
34	906.5	58.4	308	5	O8WVR6 O8WVR6 nyctotherus
35	905.5	58.3	301	5	O25692 O25692 plasmodium
36	904.5	58.2	301	5	O26006 O26006 plasmodium
37	841.5	54.2	170	6	O9XS69 O9XS69 sus scrofa
38	772	49.7	306	5	O18683 O18683 caenorhabd
39	757.5	48.8	305	3	O9P8M1 O9P8M1 yarrowia li
40	750.5	48.3	307	5	O76286 O76286 trypanosoma
41	748.5	48.2	303	3	O74260 O74260 candida par
42	746.5	48.1	379	10	O49447 O49447 arabidopsis
43	745.5	48.0	326	5	P91270 P91270 caenorhabd
44	743.5	47.9	307	5	O26697 O26697 trypanosoma
45	743	47.8	302	3	O8J0M2 O8J0M2 yarrowia li

ALIGNMENTS

RESULT 1

ID	O46373	PRELIMINARY;	PRT;	298 AA.
AC	O46373;			
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	ADP/ATP translocase.			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI_TaxID=9986;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skeletal muscle;			
RA	Yamaguchi N., Kasai M.;			
RT	*Identification of a 30kDa calsequestrin-binding protein, which			
RT	regulates calcium release from sarcoplasmic reticulum of rabbit			
RT	skeletal muscle.*;			
RL	J. Biochem. 335:541-547(1998).			
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.			
DR	EMBL; AB009386; BAA23777.1; -			
DR	InterPro: IPR001993; Mitoch_carrier.			
DR	InterPro: IPR002067; Mit_carrier.			
DR	InterPro: IPR002030; Mit_uncoupling.			
DR	Pfam; PF00153; mito_carr; 3.			
DR	PRINTS; PR00926; MITOCARRIER.			
DR	PRINTS; PR00784; MTUNCOUPLING.			
DR	PROSITE; PS00215; MITOCH_CARRIER; 3.			
KW	Membrane; Transmembrane; Transport.			
SQ	SEQUENCE 298 AA; 32901 MW; CAER32C88164AD78 CRC64;			

Qy	1 MGDHMSFLKDFLAGAFAAASKTAAPIERVKLLQVHASKQISAEKQYGIIDCVRR 60
Db	1 MSDQALSPFLKDFLAGAFAAASKTAAPIERVKLLQVHASKQISAEKQYGIIDCVRR 60
Matches	282; Conservative 7; Mismatches 8; Indels 1; Gaps 1;
Query Match	Score 1464.5; DB 6; Length 298;
Best Local Similarity	94.6%; Pred. No. 7.2e-129;


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OY 61 IPKOGFLSWRGNLANVIRYPTQALNFAFKDYKQLEFLGVDNRHKOFRYFAGN1ASG 120
    |||||||
DB 61 IPKOGFLSWRGNLANVIRYPTQALNFAFKDYKQLEFLGVDNRHKOFRYFAGN1ASG 120
OY 121 GAAGATSLCFVYPLDFARTLADVGR - RAOREFHGIDCIIFKFSKGRLGYOGFNVS 179
    |||||||
DB 121 GAAGATSLCFVYPLDFARTLADVGR - RAOREFHGIDCIIFKFSKGRLGYOGFNVS 180
OY 180 VOGIIIRAAVFGVYDTAKGMLPDPKNVHIFVSMIAQSYAVAGLSYEPDVRRRMM 239
    |||||||
DB 181 VOGIIIRAAVFGVYDTAKGMLPDPKNVHIFVSMIAQSYAVAGLSYEPDVRRRMM 240
OY 240 QSGRKADIMYTGTVDCWKRIADGAKAFKFGAMSIVLKGMGAFVLYLDEIKKYV 297
    |||||||
DB 241 QSGRKADIMYTGTVDCWKRIADGAKAFKFGAMSIVLKGMGAFVLYLDEIKKYV 298

RESULT 2
O8BV19 PRELIMINARY; PRT; 298 AA.
AC O8BV19;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DE Solute carrier family 25.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL: AK078077; BAC37117.1; -
SQ SEQUENCE 298 AA; 32904 MW; F94C89009836710B CRC64;

Query Match 94.2%; Score 1462.5; DB 11; Length 298;
Best Local Similarity 94.0%; Pred. No. 1,1e-128;
Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

OY 1 MGDHANSFLKDLGAVAAVSKTAAPIERVKLLQVHASKQISAERKYGIIIDCVR 60
    |||||||
DB 1 MGDHANSFLKDLGAVAAVSKTAAPIERVKLLQVHASKQISAERKYGIIIDCVR 60
OY 61 IPKOGFLSWRGNLANVIRYPTQALNFAFKDYKQLEFLGVDNRHKOFRYFAGN1ASG 120
    |||||||
DB 61 IPKOGFLSWRGNLANVIRYPTQALNFAFKDYKQLEFLGVDNRHKOFRYFAGN1ASG 120
OY 121 GAAGATSLCFVYPLDFARTLADVGR - RAOREFHGIDCIIFKFSKGRLGYOGFNVS 179
    |||||||
DB 121 GAAGATSLCFVYPLDFARTLADVGR - RAOREFHGIDCIIFKFSKGRLGYOGFNVS 180
OY 180 VOGIIIRAAVFGVYDTAKGMLPDPKNVHIFVSMIAQSYAVAGLSYEPDVRRRMM 239
    |||||||
DB 181 VOGIIIRAAVFGVYDTAKGMLPDPKNVHIFVSMIAQSYAVAGLSYEPDVRRRMM 240
OY 240 QSGRKADIMYTGTVDCWKRIADGAKAFKFGAMSIVLKGMGAFVLYLDEIKKYV 297
    |||||||
DB 241 QSGRKADIMYTGTVDCWKRIADGAKAFKFGAMSIVLKGMGAFVLYLDEIKKYV 298

RESULT 3
O8SOH5 PRELIMINARY; PRT; 298 AA.
AC O8SOH5;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)

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DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Adenine nucleotide translocator 2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
RN NCBI_TaxID=9913;
RP SEQUENCE FROM N.A.
RA Yamazaki N., Shinohara Y., Tanida K., Terada H.;
RT "Structural properties of mammalian mitochondrial ADP/ATP carriers:
RT identification of possible amino acids that determine functional
RT differences in its isoforms.";
RL Mitochondrion 1:371-379(2002).
DR EMBL: AB065433; BAB84673.1; -
DR InterPro: IPR001993; Mitoch. carrier.
DR Pfam: PF00153; mito. carr. 3.
DR PROSITE: PS00215; MITOCH_CARRIER_3.
SQ SEQUENCE 298 AA; 32935 MW; CB6897BB987B79C0 CRC64;

Query Match 90.9%; Score 1411.5; DB 6; Length 298;
Best Local Similarity 89.9%; Pred. No. 6,6e-124;
Matches 267; Conservative 16; Mismatches 13; Indels 1; Gaps 1;

OY 1 MGDHANSFLKDLGAVAAVSKTAAPIERVKLLQVHASKQISAERKYGIIIDCVR 60
    |||||||
DB 1 MTDAAVSFANDFLAGVAAAIKSTAAPIERVKLLQVHASKQITADKQYKGIIDCVR 60
OY 61 IPKOGFLSWRGNLANVIRYPTQALNFAFKDYKQLEFLGVDNRHKOFRYFAGN1ASG 120
    |||||||
DB 61 IPKOGFLSWRGNLANVIRYPTQALNFAFKDYKQLEFLGVDNRHKOFRYFAGN1ASG 120
OY 121 GAAGATSLCFVYPLDFARTLADVGR - AOREFHGIDCIIFKFSKGRLGYOGFNVS 179
    |||||||
DB 121 GAAGATSLCFVYPLDFARTLADVGR - AOREFHGIDCIIFKFSKGRLGYOGFNVS 180
OY 180 VOGIIIRAAVFGVYDTAKGMLPDPKNVHIFVSMIAQSYAVAGLSYEPDVRRRMM 239
    |||||||
DB 181 VOGIIIRAAVFGVYDTAKGMLPDPKNVHIFVSMIAQSYAVAGLSYEPDVRRRMM 240
OY 240 QSGRKADIMYTGTVDCWKRIADGAKAFKFGAMSIVLKGMGAFVLYLDEIKKYV 296
    |||||||
DB 241 QSGRKADIMYTGTVDCWKRIADGAKAFKFGAMSIVLKGMGAFVLYLDEIKKYV 297

RESULT 4
O8AVM3 PRELIMINARY; PRT; 298 AA.
AC O8AVM3;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DE ATP/ADP antiporter.
GN AVANT.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN NCBI_TaxID=9031;
RP SEQUENCE FROM N.A.
RA Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba Y.;
RT "Cold-induced mitochondrial uncoupling and expression of chicken ucp
RT and ANT mRNA in chicken skeletal muscle.";
RL FEBS Lett. 0:0-0(2002).
DR EMBL: AB088686; BAC15533.1; -
SQ SEQUENCE 298 AA; 32847 MW; 1174CCEC400A10D CRC64;

Query Match 89.7%; Score 1392.5; DB 13; Length 298;
Best Local Similarity 88.3%; Pred. No. 4e-122;
Matches 263; Conservative 18; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHANSFLKDLGAVAAVSKTAAPIERVKLLQVHASKQISAERKYGIIIDCVR 60

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Db 1 MADAISFLKDFLAGVAAAIKTAAPATIERVKLLLOVHASKOIAADKOKGIIDCVR 60
QY 1PKEOGFLSFWRGNLAVIRYPTQALNFAFKDKYKOLFGVDRHKOFRYFAGNLASG 120
Db 61 IPKOGVLSFWRGNLAVIRYPTQALNFAFKDKYKOLFGVDRHKOFRYFAGNLASG 120
QY 121 GAAGATSLCFYPPDFAFTRILADYGR- AOREFHGLDCCIIRKSDGLKGLYOGFNVS 179
Db 121 GAAGATSLCFYPPDFAFTRILADYGRKAGADREFSGLDCLVKTIKSDGLKGLYOGFNVS 180
QY 180 VOGIITIRAAVFGYIDTAAGMLPDPKRNHIFVSMIAOSVAVAGLSTYPTDYRRMM 239
Db 181 VOGIITIRAAVFGYIDTAAGMLPDPKRNHIFVSMIAOSVAVAGVSYPTDYRRMM 240
QY 240 QSGRKGADIMYTGIVDCWKRIAKDEGAKAFKAGMSNVLRGMGAFVLYLDEIRKYV 297
Db 241 QSGRKGADIMYTGIVDCWKRIAKDEGAKAFKAGMSNVLRGMGAFVLYLDEIRKYV 298

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RESULT 5

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QYIC4 PRELIMINARY: PRT: 298 AA.
AC 09YIC4: MEDLINE-99083429; Pubmed-9866197;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Wrinkled frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99083429; Pubmed-9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes of
RT z, w, x, and y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008462; BAA36512.1;
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;

```

Query Match 88.7%; Score 1377.5; DB 13; Length 298;
 Best Local Similarity 86.6%; Pred. No. 1e-120;
 Matches 258; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

```

QY 1 MGDHMSFLKDFLAGVAAAVSKTAVAPIERVKLLLOVHASKOISAEKOKGIIDCVR 60
Db 1 MTDAAISRAKDFLAGVAAAIKTAAPATIERVKLLLOVHASKOITADKOKGIMDCVVR 60
QY 61 IPKEOGFLSFWRGNLAVIRYPTQALNFAFKDKYKOLFGVDRHKOFRYFAGNLASG 120
Db 61 IPKOGVLSFWRGNLAVIRYPTQALNFAFKDKYKOLFGVDRHKOFRYFAGNLASG 120
QY 121 GAAGATSLCFYPPDFAFTRILADYGR- AOREFHGLDCCIIRKSDGLKGLYOGFNVS 179
Db 121 GAAGATSLCFYPPDFAFTRILADYGRKAGADREFSGLDCLVKTIKSDGLKGLYOGFNVS 180
QY 180 VOGIITIRAAVFGYIDTAAGMLPDPKRNHIFVSMIAOSVAVAGLSTYPTDYRRMM 239
Db 181 VOGIITIRAAVFGYIDTAAGMLPDPKRNHIFVSMIAOSVAVAGVSYPTDYRRMM 240
QY 240 QSGRKGADIMYTGIVDCWKRIAKDEGAKAFKAGMSNVLRGMGAFVLYLDEIRKYV 297

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Db 241 QSGRKGADIMYTGIVDCWKRIAKDEGSAFFKAGMSNVLRGMGAFVLYLDELKYYI 298

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RESULT 6

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QYPRH1 PRELIMINARY: PRT: 298 AA.
AC 09PRH1: MEDLINE-99083429; Pubmed-9866197;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Wrinkled frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99083429; Pubmed-9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes of
RT z, w, x, and y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008463; BAA36513.1;
DR EMBL; AB008456; BAA36506.1;
DR EMBL; AB008461; BAA36511.1;
DR EMBL; AB008462; BAA36512.1;
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;

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Query Match 88.7%; Score 1377.5; DB 13; Length 298;
 Best Local Similarity 86.6%; Pred. No. 1e-120;
 Matches 258; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

```

QY 1 MGDHMSFLKDFLAGVAAAVSKTAVAPIERVKLLLOVHASKOISAEKOKGIIDCVR 60
Db 1 MTDAAISRAKDFLAGVAAAIKTAAPATIERVKLLLOVHASKOITADKOKGIMDCVVR 60
QY 61 IPKEOGFLSFWRGNLAVIRYPTQALNFAFKDKYKOLFGVDRHKOFRYFAGNLASG 120
Db 61 IPKOGVLSFWRGNLAVIRYPTQALNFAFKDKYKOLFGVDRHKOFRYFAGNLASG 120
QY 121 GAAGATSLCFYPPDFAFTRILADYGR- AOREFHGLDCCIIRKSDGLKGLYOGFNVS 179
Db 121 GAAGATSLCFYPPDFAFTRILADYGRKAGADREFSGLDCLVKTIKSDGLKGLYOGFNVS 180
QY 180 VOGIITIRAAVFGYIDTAAGMLPDPKRNHIFVSMIAOSVAVAGLSTYPTDYRRMM 239
Db 181 VOGIITIRAAVFGYIDTAAGMLPDPKRNHIFVSMIAOSVAVAGVSYPTDYRRMM 240
QY 240 QSGRKGADIMYTGIVDCWKRIAKDEGAKAFKAGMSNVLRGMGAFVLYLDEIRKYV 297
Db 241 QSGRKGADIMYTGIVDCWKRIAKDEGSAFFKAGMSNVLRGMGAFVLYLDELKYYI 298

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OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Euryarchaeta: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
 OC Actinopterygii: Neopterygii: Teleostei: Osteichthyes: Cypriniformes:
 OC Cyprinidae: Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22035902; PubMed=12006978;
 RA Golling G., Amsterdam A., Sun Z., Antonelli M., Maldonado E., Chen W.,
 RA Burgess S., Hald M., Artzt K., Farrington S., Lin S.-Y., Nissen R.M.,
 RA Hopkins N.;
 RT "Insertional mutagenesis in zebrafish rapidly identifies genes
 RT essential for early vertebrate development.";
 RL Nat. Genet. 31:135-140(2002).
 DR EMBL, AF506216; AACM34660.1; -;
 DR InterPro: IPR001993; Mitoch_carrler.
 DR InterPro: IPR002067; Mlt_carrler.
 DR InterPro: IPR002030; Mlt_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTCUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER_3.
 SO SEQUENCE 298 AA; 32763 MW; D78663CF65C51D39 CRC64;

Query Match	88.6%	Score 1375.5	DB 13	Length 298
Best Local Similarity	86.9%	Pred. No. 1.6e-120		
Matches 259	Conservative 22	Mismatches 16	Indels 1	Gaps 1

[illegible]

QY	122	GAGAAATSLCEVYPLDEARRRLAADVGR- AQQEEFGGLDCIIKIFKSSGTEGLQGGNVS	179
Db	121	GAGAAATSLCEVYPLDEARRRLAADVGRKGAEE REFGGLCNCIVKISKSDGICGLQGGNVS	180
QY	180	VGGIITTYRAAYFCEVYPTAKGMLPDDRNVHIF PSMNIAGSYAAVAGLLSLSPDDTYRRRMM	239
Db	181	VGGIITTYRAAYFCEIYDTAKGMLPDDRKNHIY SMNLIAGSYAAVAGLLSLSPDDTYRRRMM	240

Oy 240 QSGRKGDIMYGTVDCKMKIAKEGAKAFFKGAMSVLRMGAFVLVLYDEIKKYV 297
 |||||:::||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 241 QSGRKGDIMYSTIDCMKRIAREGGKAFFKGAMSVNLRMGCAFVLVLYDELKVI 298

RESULT 8

ID	09PRH2	PRELIMINARY;	PRT;	298 AA.
AC	09PRH2			
DT	01-MAY-2000 (T-EMBLrel. 13, Created)			
DT	01-MAY-2000 (T-EMBLrel. 13, Last sequence update)			
DT	01-MAY-2003 (T-EMBLrel. 23, Last annotation update)			
DE	ADP/ATP translocase.			
OS	Rana rugosa (Winkled frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.			
OX	NCBI_TaxId=8410;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99083429; PubMed=9866197;			
RA	Mura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;			
RT	"The origin and differentiation of the heteromorphic sex chromosomes			
RT	z, w, x, and y in the frog Rana rugosa, inferred from the sequences of			
RT	a sex-linked gene, ADP/ATP translocase.";			
RL	Mol. Biol. Evol. 15:1612-1619(1998).			
CC	- - SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.			
DR	EMBL; AB008460; BAA36510.1; -			
DR	EMBL; AB008458; BAA36508.1; -			
DR	EMBL; AB008459; BAA36509.1; -			

DR InterPro: IPR001993; Mitochondrion carrier.
DR InterPro: IPR002067; Mitochondrion carrier.
DR InterPro: IPR002030; Mitochondrion carrier.
DR Pfam: PF00153; Mitochondrion carrier.
DR PRINTS: PR00926; Mitochondrion carrier.
DR PRINTS: PR00784; Mitochondrion carrier.
DR PROSITE: PS00215; Mitochondrion carrier.
DR Membrane: Transmembrane; Transport.
KW Sequence: 298 AA; 33082 MW; B02225E867599A06 CRC64;

Query Match	88.5%	Score 1374.5	DB 13	Length 298
Best Local Similarity	86.2%	Pred. No. 1.9e-120		
Matches 257	Conservative 24	Mismatches 16	Indels 1	Gaps 1

[illegible]

QY	121	GAGAAATSEFPVPLDPFARFLAAADVGR - AAGEEFGLEDGCIITIKFSPGSLGKGLGVGNVS	179
Db	121	GAGAAATSEFPVPLDPFARFLAAADVGRKGAADDEFGLGDLCAKIFRSGKLGKGLGVGNVS	180
QY	180	VGGIIITTYRAATRGVYDTAKGMLPDRKNHIEVSMHIAQSVYAVAGGLSPPTDYIRRRMM	238
Db	181	VGGIIITTYRAATRGVYDTAKGMLPDRKNHIEVSMHIAQSVYAVAGGLSPPTDYIRRRMM	240

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Oy      240 QSGRKGDIMYTGTVDCWKRIAKEGAKAFKGAWSNVLRGMSGAFVLVLYDEIKKYV 297
        |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      241 QSGRKGAETMYSTIIDCMKKIARDEGSRFAFKGAWSNVLRGMSGAFVLVLYDEIKKYI 298

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RESULT 9	
ID	PRELIMINARY;
Q919M9	PRT; 298 AA.
Q919M9	
AC Q919M9:	
DT 01-OCT-2000	(TREMBLrel. 15 Created)
DT 01-OCT-2000	(TREMBLrel. 15; last sequence update)

DE Adenine nucleotide translocase.
GN AMT1.
OC xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae.
OC Xenopodinae; Xenopus.
NCBI_taxid=8335;

RP SEQUENCE FROM N.A.
RA CREWFIELD M.J., Khosrowshahian F., Yarmuza S.L., Liverage R.A.;
RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
RT Dynamic Patterns of Expression During Development."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBI databases
-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF213467; AAF63471.1; -.

DR Interp0: IPR002030; Mt_uncoupling.
DR Pfam: PF00153; mlt0_carr; 3.
DR PRINTS: PRO00926; MTCOCARRIER.
DR PRINTS: PRO00784; MTCOCUPLING.
DR PROSITE: PS00215; MTCOC_CARRIER; 3.
KW Membrane; Transmembrane; Transport.
KW SEQUENCE 238 AA; 32940 MW; 91B740133751877F CRC64

Query Match	88.0%	Score 1366.5	DB 13	Length 298
Best Local Similarity	86.2%	Pred. No. 1.1e-119		
Matches 257; Conservative	23	Mismatches 17	Indels 1	Gaps 1

09 1 MGDHWSFLDF LAGAVAAASTAVAPIERKILLQVHASKQISAEROKKGIIDCVR 600

DB 1 MTDAIAISAKDFLAGVAAASKTAVAPIERVKLLQVOHASKQITADKHKYKIMDCVVR 60
 OY 61 IPKDGSLFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRYFAGNLASG 120
 DB 61 IPKDGSLFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRYFAGNLASG 120
 OY 121 GAAGATSLCFYVPLDFARTRLAADVGRRA-QREFHGLDCCIIFKSDGLNGLYOGFNVS 179
 DB 121 GAAGATSLCFYVPLDFARTRLAADVGRRA-QREFHGLDCCIIFKSDGLNGLYOGFNVS 180
 OY 180 VGGIITRAAYFGYDTAKGMLPDPKNTPIFVSMIAQVTAAGFASYPEDTVRRMM 239
 DB 181 VGGIITRAAYFGYDTAKGMLPDPKNTPIFVSMIAQVTAAGFASYPEDTVRRMM 240
 OY 240 QSGRKGADIMYTGVDCKRIKADGAKAFKFGAMSNTLRGGAFLVLYDEIKKYV 297
 DB 241 QSGRKGADIMYTGVDCKRIKADGAKAFKFGAMSNTLRGGAFLVLYDEIKKYV 298

RESULT 10

OY95VX4 PRELIMINARY; PRT; 299 AA.
 AC O95VX4:
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE ADP-ATP translocator.
 OS Ethmostigmus rubripes.
 OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
 CC Pleurostilmophora; Scolopendromorpha; Scolopendridae; Ethmostigmus.
 OX NCBI_TaxID=62613;
 RN [1]
 RA Burnell J.N.;
 RP "Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus
 rubripes.";
 RT Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 RL EMBL; AF401758; AAL02100.1;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carri. 3.
 DR PRINTS: PR00926; MITOCH_CARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 SQ SEQUENCE 299 AA; 33037 MW; 3C3B0CB26E7C3C5E CRC64;

Query Match 80.2%; Score 1245.5; DB 5; Length 299;
 Best Local Similarity 80.3%; Pred. No. 2.3e-108;
 Matches 236; Conservative 25; Mismatches 32; Indels 1; Gaps 1;

OY 5 AWSFLKDFLAGVAAAVASKTAVAPIERVKLLQVOHASKQISAEKQYKGIIDCVVRIPKE 64
 DB 5 AWSFLKDFLAGVAAAVASKTAVAPIERVKLLQVOHASKQISAEKQYKGIIDCVVRIPKE 64
 OY 65 OGSFLFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRYFAGNLASGAG 124
 DB 65 OGSFLFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRYFAGNLASGAG 124
 OY 125 ATSLCFYVPLDFARTRLAADVGR-BAOREFHGLDCCIIFKSDGLNGLYOGFNVSOGI 183
 DB 125 ATSLCFYVPLDFARTRLAADVGR-BAOREFHGLDCCIIFKSDGLNGLYOGFNVSOGI 184
 OY 184 IIRAAAYGVYDTAKGMLPDPKNTPIFVSMIAQVTAAGFASYPEDTVRRMMQSGR 243
 DB 185 IIRAAAYGVYDTAKGMLPDPKNTPIFVSMIAQVTAAGFASYPEDTVRRMMQSGR 244
 OY 244 KGADIMYTGVDCKRIKADGAKAFKFGAMSNTLRGGAFLVLYDEIKKYV 297
 DB 245 KGADIMYTGVDCKRIKADGAKAFKFGAMSNTLRGGAFLVLYDEIKKYV 298

RESULT 11
 OY9NHWS PRELIMINARY; PRT; 300 AA.
 ID O9NHWS

AC O9NHWS;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE ADP-ATP translocase.
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OX Calliphoridae; Lucilia.
 OX NCBI_TaxID=7375;
 RN [1]
 RA SEQUENCE FROM N.A.
 RC STRAIN=SS mal seeking;
 RA Chen Z., Fair J.A., Batterham P.;
 RT "A DNA clone encoding the ADP/ATP translocase of Lucilia cuprina.";
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
 CC -1 SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AF218587; AAF32322.1;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carri. 3.
 DR PRINTS: PR00926; MITOCH_CARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Membrane; Transport.
 SQ SEQUENCE 300 AA; 33036 MW; 5459DF0EAD0E2E742 CRC64;

Query Match 79.9%; Score 1241.5; DB 5; Length 300;
 Best Local Similarity 78.7%; Pred. No. 5.6e-108;
 Matches 236; Conservative 25; Mismatches 36; Indels 3; Gaps 1;

OY 1 MGDHA---WSFLKDFLAGVAAAVASKTAVAPIERVKLLQVOHASKQISAEKQYKGIIDC 57
 DB 1 MGDHAADPLGFYKDFAGISAAVSKTAVAPIERVKLLQVOHASKQISAEKQYKGIIDC 60
 OY 58 VRIKREOGSLFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRYFAGNL 117
 DB 61 FVRIKREOGSLFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRYFAGNL 120
 OY 118 ASGGAAGATSLCFYVPLDFARTRLAADVGRBAOREFHGLDCCIIFKSDGLNGLYOGFN 177
 DB 121 ASGGAAGATSLCFYVPLDFARTRLAADVGRBAOREFHGLDCCIIFKSDGLNGLYOGFN 180
 OY 178 VSVGGIITRAAYFGYDTAKGMLPDPKNTPIFVSMIAQVTAAGFASYPEDTVRRMM 237
 DB 181 VSVGGIITRAAYFGYDTAKGMLPDPKNTPIFVSMIAQVTAAGFASYPEDTVRRMM 240
 OY 238 MMQSGRKGADIMYTGVDCKRIKADGAKAFKFGAMSNTLRGGAFLVLYDEIKKYV 297
 DB 241 MMQSGRKGADIMYTGVDCKRIKADGAKAFKFGAMSNTLRGGAFLVLYDEIKKYV 300

RESULT 12
 OY81RAO PRELIMINARY; PRT; 312 AA.
 ID O81RAO;
 AC O81RAO:
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE CG16944-PC.
 GN SE8B.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OX Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RA SEQUENCE FROM N.A.
 RP MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Cealiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazek R.G., Champagne M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA April J.F., Agbayan A., An H.J., Andrews-Pfannkuch C., Baldwin D.,
 RA Baller R.M., Baou A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Besson P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Heston D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jallat M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spletter E., Spreading A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodruff, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yen R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).

RP [2]
 RP SEQUENCE FROM N.A.
 RA Gelniker S.E., Adams M.D., Krommler B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frishe E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jallat M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phoumenavong S., Pittman G.S., Puri V., Richarde S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
 RT "Sequencing of *Drosophila melanogaster* genome."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RP [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminler J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Gelniker S.E.,
 RA Clump M., Dysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommler B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
 RT "Annotation of *Drosophila melanogaster* genome."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RP [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Gelniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.,
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RP [5]
 RP SEQUENCE FROM N.A.

RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AEO03484; AAO09267.1;
 SO SEQUENCE 312 AA; 34214 MW; 76D5634E74E168DF CRC64;

Query Match 79.9%; Score 1241; DB 5; Length 312;

Best Local Similarity 79.7%; Pred. No. 6,6e-108;
 Matches 232; Conservative 26; Mismatches 33; Indels 0; Gaps 0;
 QY 5 AMSFLKQFLGAVAAVSKTAVAPIERVKLLLOVQHASKOISAKOYKGIIDCVRRPK 64
 DB 20 AVGFVKDFPAAGGISAASKTAVAPIERVKLLLOVQHASKOISPKQYKGVDCIRPK 79
 QY 65 QGFLSPFRGNLANVIRFPQALNFAFKDKYKQFLGCVDRHKKQFWYFPGNLSGAG 124
 DB 80 QGFSFPRGNLANVIRFPQALNFAFKDKYKQFLGCVDRHKKQFWYFPGNLSGAG 139
 QY 125 ATSLCFYPLDFATRLAADVGRARORFHCGLCCITIKRSQGLRGYOGFNVSGCII 184
 DB 140 ATSLCFYPLDFATRLAADVGRARORFHCGLCCITIKRSQGLRGYOGFNVSGCII 199
 QY 185 IYRAAYGVDTAKGMLPDPKRVNIFVFMNIAQSVTVAGLSYEPFTVRRMMQSGRK 244
 DB 200 IYRAAYGVDTAKGMLPDPKRVNIFVFMNIAQSVTVAGLSYEPFTVRRMMQSGRK 259
 QY 245 GADIMYGTVDQWKRKADEGAKAFKGAWSNVLRGGAFLVLYDEIRK 295
 DB 260 ATEVIYKNTLHCMTATIKQSGTGAFFKGAWSNVLRGGAFLVLYDEIRK 310

RESULT 13
 ID Q91336 PRELIMINARY; PRT; 317 AA.
 AC Q91336;
 DT 01-NOV-1996 (TREMURel. 01, Created)
 DT 01-MAY-1999 (TREMURel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMURel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS Rana sylvatica (Wood Frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
 OX NCBI_TaxID=45438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver.
 RX MEDLINE=97398141; PubMed=9256066;
 RA Cal O., Greenway S.C., Storey K.B.;
 RT "Differential regulation of the mitochondrial ADP/ATP translocase gene
 in wood frogs under freezing stress."
 RL Biochim. Biophys. Acta 1353:69-78(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver.
 RA Cal O., Storey K.B.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: U44832; AAA97882.2;
 DR InterPro: IPR001993; Mitoch carrier.
 DR InterPro: IPR002067; Mit. carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER. 3.
 KW Membrane; Transmembrane; Transport.
 SO SEQUENCE 317 AA; 35005 MW; 5F66B7ED8D5CEB72 CRC64;

Query Match 79.5%; Score 1234.5; DB 13; Length 317;
 Best Local Similarity 85.7%; Pred. No. 2.7e-107;
 Matches 233; Conservative 21; Mismatches 17; Indels 1; Gaps 1;

QY 1 MGDHAWSELDPLAGAAVSKTAVAPIERVKLLLOVHASKOISAKOYKGIIDCVRR 60
 DB 1 MTDANSFADPLAGAAVSKTAVAPIERVKLLLOVHASKOISAKOYKGIIDCVRR 60
 QY 61 IPKEQGLSFWRGNLANVIRFPQALNFAFKDKYKQFLGCVDRHKKQFWYFPGNLSG 120
 DB 61 IPKEQGLSFWRGNLANVIRFPQALNFAFKDKYKQFLGCVDRHKKQFWYFPGNLSG 120
 QY 121 GAAGATSLCFYPLDFATRLAADVGRARORFHCGLCCITIKRSQGLRGYOGFNV 179
 DB 121 GAAGATSLCFYPLDFATRLAADVGRARORFHCGLCCITIKRSQGLRGYOGFNV 179

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 19:27:31 ; Search time 52.3919 Seconds

(without alignments)
902.821 Million cell updates/sec

Title: US-09-811-132-32

Perfect score: 1547
Sequence: 1 MTDALSFADFLAGVAAA.....LRMGCAFVLVYDEIKKYP 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
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24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
25: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1547	100.0	298	AAV71032	Human adenine nucl
2	1547	100.0	298	AAU01379	Human adenine nucl
3	1547	100.0	298	AAO10379	Human adenine nucl
4	1537	99.4	298	AAO18516	Human insulin rece
5	1454	94.0	298	AAV71033	Human adenine nucl
6	1454	94.0	298	AAK39641	Human polypeptide
7	1454	94.0	298	AAU01200	Human adenine nucl
8	1454	94.0	298	AAU01380	Human adenine nucl
9	1454	94.0	323	AAW41427	Human polypeptide

10	1417	91.6	325	22	ABG15423	Novel human diagno
11	1411	91.2	298	19	AAW61169	Anti protein. Mus
12	1409	91.1	293	22	ABU53219	Human metabolism-a
13	1391.5	89.9	297	21	AAV71031	Human adenine nucl
14	1391.5	89.9	297	22	AAU01198	Human adenine nucl
15	1391.5	89.9	297	23	AAU010378	Human adenine nucl
16	1346	87.0	263	22	ABG27056	Novel human diagno
17	1339	86.6	429	22	ABR41715	Human human diagno
18	1253.5	81.0	299	22	ABB66082	Drosophila melanog
19	1253.5	81.0	299	22	ABB67300	Drosophila melanog
20	1125.5	72.8	307	22	ABBS5380	Drosophila melanog
21	1102	71.2	315	22	ABU53218	Human metabolism-a
22	1102	71.2	315	23	AAE21175	Human TRICH-19 pro
23	988	63.9	228	23	ABP43205	Human ovarian anti
24	923	59.7	222	23	ABP4106	Human TRICH SEQ ID
25	895.5	57.9	298	22	ABG18922	Novel human diagno
26	792	51.2	484	22	ABG15422	Novel human diagno
27	792	51.2	484	22	ABG27055	Novel human diagno
28	779.5	50.4	301	23	ABP73357	Candida albicans e
29	747.5	48.3	346	21	AAG36577	Arabidopsis thalia
30	747.5	48.3	346	21	AAG37261	Arabidopsis thalia
31	747.5	48.3	346	21	AAG37264	Arabidopsis thalia
32	747.5	48.3	346	21	AAG38460	Arabidopsis thalia
33	747.5	48.3	363	21	AAG36576	Arabidopsis thalia
34	747.5	48.3	363	21	AAG37260	Arabidopsis thalia
35	747.5	48.3	363	21	AAG37263	Arabidopsis thalia
36	747.5	48.3	363	21	AAG38459	Arabidopsis thalia
37	747.5	48.3	381	21	AAG36575	Arabidopsis thalia
38	747.5	48.3	381	21	AAG37259	Arabidopsis thalia
39	747.5	48.3	381	21	AAG37262	Arabidopsis thalia
40	747.5	48.3	381	21	AAG38458	Arabidopsis thalia
41	747.5	48.3	992	21	AAG38672	Arabidopsis thalia
42	747.5	48.3	1009	21	AAG38671	Arabidopsis thalia
43	747.5	48.3	1027	21	AAG38670	Arabidopsis thalia
44	746	48.2	379	24	ABP81267	Arabidopsis thalia
45	744.5	48.1	346	21	AAG17731	Arabidopsis thalia

ALIGNMENTS

RESULT 1	AAV71032	standard; Protein; 298 AA.
ID	AAV71032	standard; Protein; 298 AA.
XX	AAV71032;	
AC	29-AUG-2000	(first entry)
DT	29-AUG-2000	(first entry)
DE	Human adenine nucleotide translocator ANT2.	
XX	Human: adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; neuroleptic; antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; psoriasis;	
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease; dysontia; diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS;	
KW	mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;	
KW	mitochondrial diabetes and deafness; hyperproliferative disorder;	
KW	myoclonic epilepsy red ragged fibre syndrome.	
OS	Homo sapiens.	
XX	WO200026370-A2.	
PN	11-MAY-2000.	
XX	03-NOV-1999;	99WO-US25883.
PD	03-NOV-1999;	98US-0185904.
PF	03-NOV-1999;	98US-0185904.
XX	08-SEP-1999;	99US-0393441.
PR	08-SEP-1999;	99US-0393441.
XX		

PA (MITO-) MITOKOR.
 XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 XX
 DR N-PSDB; AAD00520.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 PS Claim 45; Page 172-173; 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MEAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MID), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT2 from human brain.
 CC
 XX
 SQ Sequence 298 AA;
 Query Match 100.0%; Score 1547; DB 21; Length 298;
 Best Local Similarity 100.0%; Pred. No. 2,3e-154;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTDALSPAKDFLAGVAAIAISKTAAPIERVKLLQOVHASKQITADKQYKIIDCVAR 60
 DB 1 MTDALSPAKDFLAGVAAIAISKTAAPIERVKLLQOVHASKQITADKQYKIIDCVAR 60
 QY 61 IPKEQEVLSFWNRGNLANVIRYPTQALNFAFKDKYQIFLGVDKRTQFRRYAGNLIASG 120
 DB 61 IPKEQEVLSFWNRGNLANVIRYPTQALNFAFKDKYQIFLGVDKRTQFRRYAGNLIASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADVGKAGAREFRGLGDCLVKITYSDGKIGLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVGKAGAREFRGLGDCLVKITYSDGKIGLYOGFNVS 180
 QY 181 VOGIITIRAAVREGIYDTAKGMLPDPKNTHTIVISWMTAQVTAAGLTSPFDVRRRRMM 240
 DB 181 VOGIITIRAAVREGIYDTAKGMLPDPKNTHTIVISWMTAQVTAAGLTSPFDVRRRRMM 240
 QY 241 OSGRKGTDMYTGTLDCWKRIADDEGKAFKFGAMSNTVLRGMGAVLVLYIDEIKKYYT 298
 DB 241 OSGRKGTDMYTGTLDCWKRIADDEGKAFKFGAMSNTVLRGMGAVLVLYIDEIKKYYT 298
 RESULT 2
 AA001199
 ID AA001199 standard; Protein; 298 AA.
 XX
 AC AA001199;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human adenine nucleotide translocator-2 (ANT-2) protein.
 KW Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

XX OS Homo sapiens.
 XX
 PN WO200132876-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-US30535.
 XX
 PR 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
 PI Velicelcib1 G, Davis RE;
 XX
 DR N-PSDB; AAS05902.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 PS Disclosure; Fig 2; 186pp; English.
 XX
 CC The present sequence represents human adenine nucleotide translocator-2
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 CC
 XX
 SQ Sequence 298 AA;
 Query Match 100.0%; Score 1547; DB 22; Length 298;
 Best Local Similarity 100.0%; Pred. No. 2,3e-154;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTDALSPAKDFLAGVAAIAISKTAAPIERVKLLQOVHASKQITADKQYKIIDCVAR 60
 DB 1 MTDALSPAKDFLAGVAAIAISKTAAPIERVKLLQOVHASKQITADKQYKIIDCVAR 60
 QY 61 IPKEQEVLSFWNRGNLANVIRYPTQALNFAFKDKYQIFLGVDKRTQFRRYAGNLIASG 120
 DB 61 IPKEQEVLSFWNRGNLANVIRYPTQALNFAFKDKYQIFLGVDKRTQFRRYAGNLIASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADVGKAGAREFRGLGDCLVKITYSDGKIGLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVGKAGAREFRGLGDCLVKITYSDGKIGLYOGFNVS 180
 QY 181 VOGIITIRAAVREGIYDTAKGMLPDPKNTHTIVISWMTAQVTAAGLTSPFDVRRRRMM 240
 DB 181 VOGIITIRAAVREGIYDTAKGMLPDPKNTHTIVISWMTAQVTAAGLTSPFDVRRRRMM 240
 QY 241 OSGRKGTDMYTGTLDCWKRIADDEGKAFKFGAMSNTVLRGMGAVLVLYIDEIKKYYT 298
 DB 241 OSGRKGTDMYTGTLDCWKRIADDEGKAFKFGAMSNTVLRGMGAVLVLYIDEIKKYYT 298

RESULT 3
AA010379
ID AA010379 standard; Protein; 298 AA.
XX
AC AA010379;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human adenine nucleotide translocator 2 (ANT2).
XX
KM Human; adenine nucleotide translocator; ANT; ss;
XX
KW mitochondrial matrix protein.
XX
OS Homo sapiens.
XX
PN WO200185944-A2.
XX
PD 15-NOV-2001.
XX
PF 11-MAY-2001; 2001WO-US15416.
XX
PR 11-MAY-2000; 2000US-0569327.
XX
PA (MITO-) MITOKOR.
XX
PI Anderson CM, Davys RE, Clevenger W, Willey SE, Miller SM, Szabo TR;
PI Ghosh SS, Moos WH, Pel Y, Carroll AK;
XX
DR MPI: 2002-055598/07.
DR N-PSDB; AAS16689.
XX
PT Novel recombinant expression construct for producing adenine nucleotide
PT translocator polypeptides, comprises a regulated promoter linked to
PT nucleic acid encoding the polypeptide
XX
PS Claim 44; Fig 2; 147pp; English.
XX
XX The invention relates to a recombinant expression construct (I)
CC comprising a regulated promoter operably linked to a nucleic acid
CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
CC proteins mediate the exchange of ATP synthesised in the mitochondrial
CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
CC culturing the host cell. (I) is also useful for targeting a polypeptide
CC of interest to a mitochondrial membrane, where ANT polypeptide is
CC expressed as a fusion protein with the polypeptide of interest.
CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
CC useful for identifying an agent that binds to an ANT polypeptide. ANT
CC ligand is useful for determining the presence of an ANT polypeptide,
CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
CC ANT from a biological sample, where the ANT ligand is covalently or non-
CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
CC useful for identifying an agent that interacts with an ANT polypeptide.
CC The present sequence represents the amino acid sequence of human ANT2.
XX
SQ Sequence 298 AA:

Query Match 100.0%; Score 1547; DB 23; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.3e-154;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 181 VGGIIIRAAVFGIYDFAKGMLPDPKNTHTVISMIAQVTVAVAGLTSYPDFVRRRMM 240
DB 181 VGGIIIRAAVFGIYDFAKGMLPDPKNTHTVISMIAQVTVAVAGLTSYPDFVRRRMM 240
OY 241 QSGRKGTDMYTGTLDCKWRIARDEGKAFFKGAMSNVLKMGAFVLYLDEIKRYT 298
DB 241 QSGRKGTDMYTGTLDCKWRIARDEGKAFFKGAMSNVLKMGAFVLYLDEIKRYT 298

RESULT 4
AA018516
ID AA018516 standard; Protein; 298 AA.
XX
AC AA018516;
XX
DT 11-OCT-2002 (first entry)
XX
DE Human insulin receptor signaling modifier SEQ ID NO: 54.
XX
KM Human; insulin receptor signaling; insulin receptor signaling modifier;
XX ISM; diabetes; metabolic syndrome; antidiabetic.
XX
OS Homo sapiens.
XX
PN WO200255664-A2.
XX
PD 18-JUL-2002.
XX
PF 11-JAN-2002; 2002WO-US01048.
XX
PR 12-JAN-2001; 2001US-261226P.
PR 12-JAN-2001; 2001US-261303P.
PR 12-JAN-2001; 2001US-261304P.
PR 12-JAN-2001; 2001US-261335P.
PR 12-JAN-2001; 2001US-261336P.
PR 12-JAN-2001; 2001US-261361P.
PR 12-JAN-2001; 2001US-261456P.
PR 12-JAN-2001; 2001US-261457P.
PR 12-JAN-2001; 2001US-261458P.
PR 12-JAN-2001; 2001US-261459P.
PR 12-JAN-2001; 2001US-261461P.
PR 12-JAN-2001; 2001US-261518P.
PR 12-JAN-2001; 2001US-261531P.
PR 12-JAN-2001; 2001US-261532P.
PR 12-JAN-2001; 2001US-261589P.
PR 12-JAN-2001; 2001US-261590P.
PR 12-JAN-2001; 2001US-261594P.
PR 12-JAN-2001; 2001US-261695P.
PR 12-JAN-2001; 2001US-261697P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Seidel-Dugan C, Ferguson KC, Kidd T;
PI N-PSDB; AAL48635.
XX
PT Identifying an insulin receptor signaling modulator, useful as drug
PT targets for treating diabetes or metabolic disorders, comprises
PT contacting an assay system comprising insulin receptor signaling
PT modifiers with a test agent
XX
PS Disclosure: Page 160-161; 232pp; English.
XX
XX The present invention relates to a method of identifying a candidate
CC insulin receptor (INR) signaling modulating agent, involving contacting
CC an assay system comprising an insulin receptor signaling modifier (ISM)
CC polypeptide or nucleic acid with a test agent, and detecting a test
CC agent-biased activity of the assay system. The method is useful for
CC identifying candidate INR signaling modulating agents. ISM genes may be
CC used as drug targets for treatment of disorders related to INR signaling
CC such as diabetes or metabolic syndrome. ISM nucleic acids and
CC polypeptides are useful for identifying and testing agents that modulate

CC ISM function and for other applications related to the involvement of ISM
CC in INR signaling, and for identifying subjects having a predisposition to
CC such diseases associated with INR signaling. The present sequence is an
CC ISM protein described in the exemplification of the invention.

SO Sequence 298 AA;

Query Match 99.4%; Score 1537; DB 23; Length 298;
Best Local Similarity 99.3%; Pred. No. 2,6e-153;
Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTDALSFANDFLAGVAAAIKSTAVAPIERVKLLLOVHASKQITADKQKGIIDCVR 60
DB 1 MTDAAVFAFADFLAGVAAAIKSTAVAPIERVKLLLOVHASKQITADKQKGIIDCVR 60
QY 61 IPKEOVLSEFMRGNLANVIRFPTQALNFAEKDKYKQIFLGGVDRKTFQMRFFAGNLSG 120
DB 61 IPKEOVLSEFMRGNLANVIRFPTQALNFAEKDKYKQIFLGGVDRKTFQMRFFAGNLSG 120
QY 121 GAAGATSLCFVYPLDFARTRLADVKGAGEREERGLGDCLVKTKSDGKIGLYQGFNVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADVKGAGEREERGLGDCLVKTKSDGKIGLYQGFNVS 180
QY 181 VOGIITIRAAVFGIYDPAKGLPDPKNTHTVISMIAQTYAVAGLSTYPTDVRRRMM 240
DB 181 VOGIITIRAAVFGIYDPAKGLPDPKNTHTVISMIAQTYAVAGLSTYPTDVRRRMM 240
QY 241 QSGRKGTDIMYTGTLDCMRKIARDEGKAFKFGKMSVNLGMSGAFVLYLYDEIKRYT 298
DB 241 QSGRKGTDIMYTGTLDCMRKIARDEGKAFKFGKMSVNLGMSGAFVLYLYDEIKRYT 298

RESULT 5

AAV71033 standard; Protein: 298 AA.

AC AAV71033;
DT 29-AUG-2000 (first entry)
DE Human adenine nucleotide translocator ANT3.

KW Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
KW adenosine diphosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW mitochondrial permeability transition; neuroprotective; neuroleptic;
KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW Alzheimer's disease; cerebroprotective; therapeutic; screening; psoriasis;
KW diabetes; leber's hereditary optic neuropathy; Huntington's disease; dystonia;
KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
KW mitochondrial diabetes and deafness; hyperproliferative disorder;
KW myoclonic epilepsy red ragged fibre syndrome.

XX Homo sapiens.

PN WO200026370-A2.

PD 11-MAY-2000.

PF 03-NOV-1999; 99WO-US25883.

PR 03-NOV-1998; 98US-0185904.

PR 08-SEP-1999; 99US-0393441.

PA (MITO-) MITOKOR.

PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;

PI Ghosh SS;

DR MPI; 2000-365619/31.

DR N-PSDB; AAD00521.

XX Recombinant construct encoding adenine nucleotide translocator

PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease

PS Claim 46; Page 173-174; 175pp; English.

CC The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC diphosphate across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT3 from human brain.

XX Sequence 298 AA;

Query Match 94.0%; Score 1454; DB 21; Length 298;
Best Local Similarity 92.6%; Pred. No. 1.4e-144;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTDALSFANDFLAGVAAAIKSTAVAPIERVKLLLOVHASKQITADKQKGIIDCVR 60
DB 1 MTDAAVFAFADFLAGVAAAIKSTAVAPIERVKLLLOVHASKQITADKQKGIIDCVR 60
QY 61 IPKEOVLSEFMRGNLANVIRFPTQALNFAEKDKYKQIFLGGVDRKTFQMRFFAGNLSG 120
DB 61 IPKEOVLSEFMRGNLANVIRFPTQALNFAEKDKYKQIFLGGVDRKTFQMRFFAGNLSG 120
QY 121 GAAGATSLCFVYPLDFARTRLADVKGAGEREERGLGDCLVKTKSDGKIGLYQGFNVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADVKGAGEREERGLGDCLVKTKSDGKIGLYQGFNVS 180
QY 181 VOGIITIRAAVFGIYDPAKGLPDPKNTHTVISMIAQTYAVAGLSTYPTDVRRRMM 240
DB 181 VOGIITIRAAVFGIYDPAKGLPDPKNTHTVISMIAQTYAVAGLSTYPTDVRRRMM 240
QY 241 QSGRKGTDIMYTGTLDCMRKIARDEGKAFKFGKMSVNLGMSGAFVLYLYDEIKRYT 296
DB 241 QSGRKGTDIMYTGTLDCMRKIARDEGKAFKFGKMSVNLGMSGAFVLYLYDEIKRYT 296

RESULT 6

AAV39641 standard; Protein: 298 AA.

AC AAV39641;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 2786.

KW Human; neurotrophic; immunosuppressant; cytosolic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX Homo sapiens.

PN WO200153312-A1.

PD 26-JUL-2001.

PF 26-DEC-2000; 2000MO-US34263.
 XX
 XX 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Weinman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR MPI: 2001-442253/47.
 DR N-PSDB: AA158797.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 PS Example 4: SEQ ID NO 2786; 10078bp; English.
 XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AA158642-AA162213) with nootropic,
 CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localized neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 CC
 XX Sequence 298 AA:
 SQ
 Query Match 94.0%; Score 1454; DB 22; Length 298;
 Best Local Similarity 92.6%; Pred. No. 1.4e-144;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTDALSFADKPLAGVAAIAISTAVAPIERVKLLQVOHASKQITADKQYKGIIDCVVR 60
 DB 1 MTEQAISFADKPLAGVAAIAISTAVAPIERVKLLQVOHASKQITADKQYKGIIDCVVR 60
 QY 1 PREQEVLSFWRNGLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRYRAGNLASG 120
 DB 1 IREQGVLSFWRNGLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRYRAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADYKAGAEERFGLGDCLVITYKSDGKGLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADYKAGAEERFGLGDCLVITYKSDGKGLYOGFNVS 180
 QY 181 VGGITTYRAAYGITYTAKGMLDPKNTHTIVISWMAIQVYTAAGLTSPTDFVRRRMM 240
 DB 181 VGGITTYRAAYGITYTAKGMLDPKNTHTIVISWMAIQVYTAAGLTSPTDFVRRRMM 240
 QY 241 OSGRKGTDMYGTGLDCKMRIAIDEGKAFKFGAMSNVIRGMCAGFVLYYDEIKK 296
 DB 241 OSGRKGTDMYGTGLDCKMRIAIDEGKAFKFGAMSNVIRGMCAGFVLYYDEIKK 296
 XX
 RESULT 7
 AAU01200 standard; Protein; 298 AA.

AC AAU01200;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human adenine nucleotide translocator-3 (ANT-3) protein.
 XX
 KW Human: adenine nucleotide translocator-3; ANT-3; MPT; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200132876-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000MO-US30535.
 XX
 PR 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Murphy AN, Cleveenger W, Willey SE, Andreyev AY, Frliger LG;
 PI Velicelcbl G, Davis RE;
 XX
 DR MPI: 2001-291054/30.
 DR N-PSDB: AAS05903.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 PS Disclosure; Fig 2; 186bp; English.
 XX
 CC The present sequence represents human adenine nucleotide translocator-3
 CC (ANT-3) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 CC
 XX Sequence 298 AA:
 SQ
 Query Match 94.0%; Score 1454; DB 22; Length 298;
 Best Local Similarity 92.6%; Pred. No. 1.4e-144;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTDALSFADKPLAGVAAIAISTAVAPIERVKLLQVOHASKQITADKQYKGIIDCVVR 60
 DB 1 MTEQAISFADKPLAGVAAIAISTAVAPIERVKLLQVOHASKQITADKQYKGIIDCVVR 60
 QY 1 PREQEVLSFWRNGLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRYRAGNLASG 120
 DB 1 IREQGVLSFWRNGLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRYRAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADYKAGAEERFGLGDCLVITYKSDGKGLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADYKAGAEERFGLGDCLVITYKSDGKGLYOGFNVS 180

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QY      181  VGGIIITRAAEEGLYDFAKGMLPDPKNTHTIVISMNIAQVTAVAGLSYEPEDTVRRMM 240
      |||||
Db      181  VGGIIITRAAEEGLYDFAKGMLPDPKNTHTIVISMNIAQVTAVAGVSYEPEDTVRRMM 240
QY      241  QSGRRGTDIMYTGILDCMRKRTARDEGKAPFKGAMSNVLRMGAFVLVLYDELKK 296
      |||||
Db      241  QSGRRGADIMYTGIVDCMRKRTARDEGKAPFKGAMSNVLRMGAFVLVLYDELKK 296

RESULT 8
AAU10380
ID      AAU10380 standard; Protein: 298 AA.
AC      AAU10380;
DE      14-FEB-2002 (first entry)
XX
XX      Human adenine nucleotide translocator 3 (ANT3).
XX
XX      Human; adenine nucleotide translocator; ANT;
XX      mitochondrial matrix protein.
XX
XX      Homo sapiens.
XX
XX      WO200185944-A2.
XX
XX      15-NOV-2001.
XX
XX      11-MAY-2001; 2001WO-US15416.
XX
XX      11-MAY-2000; 2000US-0569327.
XX
XX      (MITO-) MITOKOR.
XX
XX      Anderson CM, Davis RE, Cleverger W, Wiley SE, Miller SM, Szabo TR;
XX      Ghosh SS, Moos WH, Pei Y, Carroll AK;
XX      N-PSDB; AAS16690.
XX
XX      Novel recombinant expression construct for producing adenine nucleotide
XX      translocator polypeptides, comprises a regulated promoter linked to
XX      nucleic acid encoding the polypeptide
XX
XX      Example 3; Fig 2; 147pp; English.
XX
XX      The invention relates to a recombinant expression construct (I)
XX      comprising a regulated promoter operably linked to a nucleic acid
XX      encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
XX      proteins mediate the exchange of ATP synthesised in the mitochondrial
XX      matrix for ADP in the cytosol. (I) is useful for producing recombinant
XX      ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
XX      culturing the host cell. (I) is also useful for targeting a polypeptide
XX      of interest to a mitochondrial membrane, where ANT polypeptide is
XX      expressed as a fusion protein with the polypeptide of interest.
XX      Recombinant ANT polypeptide, or cells expressing the polypeptide, is
XX      useful for identifying an agent that binds to an ANT polypeptide. ANT
XX      ligand is useful for determining the presence of an ANT polypeptide,
XX      preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
XX      ANT from a biological sample, where the ANT ligand is covalently or non-
XX      covalently bound to a solid phase. Detectably labeled ANT ligand is also
XX      useful for identifying an agent that interacts with an ANT polypeptide.
XX      The present sequence represents the amino acid sequence of human ANT3.
XX
SQ      Sequence 298 AA;

```

```

Db      1  MTEQALISFANDFLAGGIAAIAISKTAAVPIERVKLLLOVHASKQIAADKQYKGIIVDCVR 60
QY      61  IPKEQVLESEFRGNLANVIRFPTQALNFAFKDKYKQIFLGVDYKRTQFMRFAGNLSAG 120
      |||||
Db      61  IPKEQVLSFVRGNLANVIRFPTQALNFAFKDKYKQIFLGVDYKRTQFMRFAGNLSAG 120
QY      121  GAAGATSLCEFYYPPLDFARTRLAADVGRAGAREFERGLDCLVKTYSKDGKIGLYQGFNVS 180
      |||||
Db      121  GAAGATSLCEFYYPPLDFARTRLAADVGRAGAREFERGLDCLVKTYSKDGKIGLYQGFNVS 180
QY      181  VGGIIITRAAEEGLYDFAKGMLPDPKNTHTIVISMNIAQVTAVAGLSYEPEDTVRRMM 240
      |||||
Db      181  VGGIIITRAAEEGLYDFAKGMLPDPKNTHTIVISMNIAQVTAVAGVSYEPEDTVRRMM 240
QY      241  QSGRRGTDIMYTGILDCMRKRTARDEGKAPFKGAMSNVLRMGAFVLVLYDELKK 296
      |||||
Db      241  QSGRRGADIMYTGIVDCMRKRTARDEGKAPFKGAMSNVLRMGAFVLVLYDELKK 296

RESULT 9
AAM41427
ID      AAM41427 standard; Protein: 323 AA.
AC      AAM41427;
DE      22-OCT-2001 (first entry)
XX
XX      Human polypeptide SEQ ID NO 6358.
XX
XX      Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX      peripheral nervous system; neuropathy; central nervous system; CNS;
XX      Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX      amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX      chemokine; thrombolytic; drug screening; arthritis; inflammation;
XX      leukaemia.
XX
XX      Homo sapiens.
XX
XX      WO200153312-A1.
XX
XX      26-JUL-2001.
XX
XX      26-DEC-2000; 2000WO-US34263.
XX
XX      21-JAN-2000; 2000US-0488725.
XX      25-APR-2000; 2000US-0552317.
XX      09-JUL-2000; 2000US-0598042.
XX      19-JUL-2000; 2000US-0620312.
XX      03-AUG-2000; 2000US-0653450.
XX      14-SEP-2000; 2000US-0662191.
XX      19-OCT-2000; 2000US-0693036.
XX      29-NOV-2000; 2000US-0727344.
XX
XX      (HSE-) HYSEQ INC.
XX
XX      Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX      Wang J, Wang Z, Wehrman T, Xu C, Xue AD, Yang Y, Zhang J;
XX      Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX      WPI; 2001-442253/47.
XX      N-PSDB; AAI60583.
XX
XX      Novel nucleic acids and polypeptides, useful for treating disorders
XX      such as central nervous system injuries
XX
XX      Example 2; SEQ ID NO 6358; 10078pp; English.
XX
XX      The invention relates to human nucleic acids (AA157798-AA161369) and
XX      the encoded polypeptides (AAM38642-AAM42213) with nootropic,
XX      immunosuppressant and cytostatic activity. The polynucleotides are useful
XX      in gene therapy. A composition containing a polypeptide or polynucleotide
XX      of the invention may be used to treat diseases of the peripheral nervous
XX      system, such as peripheral nervous injuries, peripheral neuropathy and

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localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic CC and thrombolytic activity, cancer diagnosis and therapy, drug screening, CC assays for receptor activity, arthritis and inflammation, leukemias and CC C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed specification.

CC
XX
SQ Sequence 323 AA;

Query Match 94.0%; Score 1454; DB 22; Length 323;
Best Local Similarity 92.6%; Pred. No. 1.6e-144;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTDAAISFANDFLAGVAAAIKTAIVAPIERVKLLQVHASKQITADKQYKGIIDCYVR 60
||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 26 MTEQAISFANDFLAGVAAAIKTAIVAPIERVKLLQVHASKQITADKQYKGIIDCYVR 85

QY 61 IPKQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 86 IPKQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 145

QY 121 GAAGATSLCFYYPIDFARTRLAADYGRKAGAEFERFGIDCLVKTKYKSGIKLYOGFVNS 180
||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 146 GAAGATSLCFYYPIDFARTRLAADYGRKAGAEFERFGIDCLVKTKYKSGIKLYOGFVNS 205

QY 181 VGGIIIRAAVFGIYDPAKGMLPDPKNTNHIYSMAIAQTVAVAGLTSYPTDVARRRMM 240
||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 206 VGGIIIRAAVFGIYDPAKGMLPDPKNTNHIYSMAIAQTVAVAGLTSYPTDVARRRMM 265

QY 241 OSGRKGTIDIMYTGTLDCWKRKIARDEGKAFKAGMSNVLRGMGAFVLYLDELTK 296
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
DB 266 OSGRKGTIDIMYTGTLDCWKRKIARDEGKAFKAGMSNVLRGMGAFVLYLDELTK 321

RESULT 10
ABG15423
ID ABG15423 standard; Protein: 325 AA.
AC ABG15423;
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #15414.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PE 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
XX
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
XX
DR N-PSDB; AAS79610.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity

XX
PS Claim 20; SEQ ID No 45782; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (II) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at http://wipo.int/pub/published_pct_sequences.

CC
XX
SQ Sequence 325 AA;

Query Match 91.6%; Score 1417; DB 22; Length 325;
Best Local Similarity 92.7%; Pred. No. 1.3e-140;
Matches 280; Conservative 3; Mismatches 15; Indels 4; Gaps 3;

QY 1 MTDAAISFANDFLAGVAAAIKTAIVAPIERVKLLQVHASKQITADKQYKGIIDCYVR 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 24 MTDAAISFANDFLAGVAAAIKTAIVAPIERVKLLQVHASKQITADKQYKGIIDCYVR 83

QY 61 IPKQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 84 IPKQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 143

QY 121 GAAGATSLCFYYPIDFARTRLAADYGRKAGAEFERFGIDCLVKTKYKSGIKLYOGFVNS 180
||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 144 GAAGATSLCFYYPIDFARTRLAADYGRKAGAEFERFGIDCLVKTKYKSGIKLYOGFVNS 203

QY 181 VGGIIIRAAVFGIYDPAKGMLPDPKNTNHIYSMAIAQTVAVAGLTSYPTDVARRR 237
||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 204 VGGIIIRAAVFGIYDPAKGMLPDPKNTNHIYSMAIAQTVAVAGLTSYPTDVARRR 263

QY 238 MMOSGRKGTIDIMYTGTLDCWKRKIARDEGKAFKAGMSNVLRGMGAFVLYLDELTK 296
||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 264 EXMOGRKGTIDIMYTGTLDCWKRKIARDEGKAFKAGMSNVLRGMGAFVLYLDELTK 323

QY 297 YT 298
||
DB 324 YT 325

RESULT 11
AAM61169
ID AAM61169 standard; Protein: 298 AA.
AC AAM61169;
DT 28-SEP-1998 (first entry)
XX
DE Anti protein.
XX
KW Anti; Adenine nucleotide translocator; cloning; screening;
KW DNA Tag diodeoxy terminator cycle sequencing; oxidative phosphorylation;
KW probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;
KW hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;
KW lactic acidosis; degenerative muscle disease.
XX
OS Mus sp.

XX WO9819714-A1.
PN 14-MAY-1998.
XX
XX 31-OCT-1997; 97MO-US19882.
XX
XX 01-NOV-1996; 96US-0030017.
XX
XX (UYEM-) UNIV EMORY.
XX
XX Graham BC, Macgregor GR, Wallace DC;
PI WPI; 1998-286608/25.
DR N-PSDB; AAV36479.
XX
XX Mice lacking heart-muscle adenine nucleotide translocator protein -
PT useful as model for mitochondrial myopathy and hypertrophic
PT cardiomyopathy in animals and to test therapeutic compositions or
PT gene therapies
XX
XX Disclosure; Page 39-40; 61pp; English.
XX
XX The present sequence is the mouse Ant1 protein, the cDNA producing this
CC polypeptide is cloned by screening a mouse heart cDNA library with the
CC human Ant1 cDNA as a probe. The Ant1 cDNA sequence was determined by DNA
CC Tag diideoxy terminator cycle sequencing. The Ant1 protein is encoded by
CC the Ant1 locus, a nuclear gene on chromosome 8. This protein is required
CC in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP
CC which can then be converted into ATP. An Ant1 homozygous mutant would
CC thus be defective in OXPHOS which results in disease in oxidative
CC metabolism dependent tissues. This mouse Ant1 homozygous mutant can be
CC used as a model system for fascioscapular humeral muscular dystrophy,
CC hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model
CC systems can be used to test possible therapeutic compounds which
CC increase/mediate ATP and ADP exchange across the mitochondrial membrane
CC independent of Ant1.
XX
XX Sequence 298 AA:
SQ
Query Match 91.2%; Score 1411; DB 19; Length 298;
Best Local Similarity 89.2%; Pred. No. 4.9e-140;
Matches 265; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKQYGIIDCVVR 60
DB 1 MGDAALSPKDFLAGGIAAAVSKTAAVAPIERVKLLQVQHASKQISAEKQYGIIDCVVR 60
QY 61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFRAGNLASG 120
DB 61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFRAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLADAVGKAGAREFRGLGDLVKIYKSDGKIGLYGFNVS 180
DB 121 GAAGATSLCFVYPLDFARTLADAVGKAGAREFRGLGDLVKIYKSDGKIGLYGFNVS 180
QY 181 VGGIITIRAAVFEVYDTAKGMLDPKKNTHIIVSMIAQSVTAAGLVSPFDVRRMM 240
DB 181 VGGIITIRAAVFEVYDTAKGMLDPKKNTHIIVSMIAQSVTAAGLVSPFDVRRMM 240
QY 241 OSGRKGTDMYTGTLDCWKRIADDEGKAFKGAWSNVLRGKGAFVLYLYDEIKKY 297
DB 241 OSGRKGTDMYTGTLDCWKRIADDEGKAFKGAWSNVLRGKGAFVLYLYDEIKKY 297
RESULT 12
ABU53219 standard; Protein; 293 AA.
XX
XX ABU53219;
AC
XX
XX 14-APR-2003 (first entry)
DT
XX

DE Human metabolism-associated DKFZphes3_35f12 homologue #1.
XX
XX Human; gene therapy; vaccine; disease treatment; detection.
XX
XX Homo sapiens.
OS
XX WO200112659-A2.
XX
XX 22-FEB-2001.
PD
XX
XX 18-AUG-2000; 2000WO-IB01496.
PF
XX 18-AUG-1999; 99US-0149499.
PR 28-SEP-1999; 99US-0156503.
XX
XX (GEHU-) GERMAN HUMAN GENOME PROJECT.
PA
XX
XX Wiemann S;
PI
XX
XX WPI; 2001-327840/34.
DR
XX
XX Nucleic acids having the sequences of clones isolated from libraries of
PT different human tissues, useful in recombinant DNA methodologies -
PT
XX
XX Example III; Page 850; 1095pp; English.
XX
XX This invention describes novel polynucleotides and polypeptides isolated
CC from human cDNA libraries which can be used for gene therapy or in
CC vaccines. The polynucleotides of the invention and antibodies encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate polypeptide expression. The products of the
CC invention may also be used to identify modulators of expression and
CC activity and to down regulate expression and activity. The antibodies of
CC the invention may also be used as diagnostic agents for detecting the
CC presence of polypeptides in samples. This sequence represents a homologue
CC of a polypeptide described in the disclosure of the invention.
XX
XX Sequence 293 AA:
SQ
Query Match 91.1%; Score 1409; DB 22; Length 293;
Best Local Similarity 90.1%; Pred. No. 7.7e-140;
Matches 264; Conservative 15; Mismatches 14; Indels 0; Gaps 0;
QY 5 ALSFANDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKQYGIIDCVVRIPKE 64
DB 1 ALSFANDFLAGGIAAAVSKTAAVAPIERVKLLQVQHASKQISAEKQYGIIDCVVRIPKE 60
QY 65 QEVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFRAGNLASGGAAG 124
DB 61 QEVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFRAGNLASGGAAG 120
QY 125 ATSLCFVYPLDFARTLADAVGKAGAREFRGLGDLVKIYKSDGKIGLYGFNVSVOGI 184
DB 121 ATSLCFVYPLDFARTLADAVGKAGAREFRGLGDLVKIYKSDGKIGLYGFNVSVOGI 180
QY 185 IYIRAAVFEVYDTAKGMLDPKKNTHIIVSMIAQSVTAAGLVSPFDVRRMMQSGR 244
DB 181 IYIRAAVFEVYDTAKGMLDPKKNTHIIVSMIAQSVTAAGLVSPFDVRRMMQSGR 240
QY 245 KGTDMYTGTLDCWKRIADDEGKAFKGAWSNVLRGKGAFVLYLYDEIKKY 297
DB 241 KGADIMYTGTLDCWKRIADDEGKAFKGAWSNVLRGKGAFVLYLYDEIKKY 293
RESULT 13
AAV71031 standard; Protein; 297 AA.
XX
XX AAV71031;
AC
XX
XX 29-AUG-2000 (first entry)
DT
XX
XX Human adenine nucleotide translocator Ant1.
DE

XX Human; adenine nucleotide translocator; ANT1; mitochondria; ADP; ATP;
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KW mitochondrial permeability transition; neuroprotective; neurotropic;
 KW antiparkinsonian; cytoskeletal; antidiabetic; anticonvulsant; neuroleptic;
 KW antipsychotic; cerebroprotective; therapeutic; screening; psoriasis;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;
 KW myoclonic epilepsy red ragged fibre syndrome.

OS Homo sapiens.

PN WO200026370-A2.

PD 11-MAY-2000.

PF 03-NOV-1999; 99WO-US25883.

PR 03-NOV-1998; 98US-0185904.

PR 08-SEP-1999; 99US-0393441.

XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;

PI Ghosh SS;

DR MPI: 2000-365619/31.

DR N-PSDB; AAD00519.

XX Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease

XX Claim 44; Page 172; 175pp; English.

XX The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT1 from human brain.

XX Sequence 297 AA;

Query Match 89.9%; Score 1391.5; DB 21; Length 297;
 Best Local Similarity 88.6%; Pred. No. 5.5e-138;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTDAALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKOITADKQYGIIDCYVR 60

DB 1 MODHAMSFLKDFLAGVAAVAASKTAVAPIERVKLLQVQHASKOISAEQYGIIDCYVR 60

QY 61 IPKEBVLSTFMRGNLANVIRYPTQALNFAFDKTKQIPLFGVDKRTQFWRFPAGNLASG 120

DB 61 IPKEBGLSTFMRGNLANVIRYPTQALNFAFDKTKQIPLFGVDKRTQFWRFPAGNLASG 120

QY 121 GAAGATSLCEFYVPLDFARTRLADYGAAREFGIGLCIATKYKSSGIIKLYGCFNVS 180

DB 121 GAAGATSLCEFYVPLDFARTRLADYGR-AREFGHGLGDCIIITKFSDELKGLYCGFNVS 179

QY 181 VGGIIYRAAYEGIYDTAKGMLDPKNTHTIVISMIAQTVAAGLTSTYPTVRRRM 240

DB 180 VGGIIYRAAYEGIYDTAKGMLDPKNTHTIVISMIAQSVTAAGLTSTYPTVRRRM 239

QY 241 QSGRGKTDIMTYGTLDCMRKIRDEGKAFEFYGANSNVIRKMGAFVLYLYEIKKY 297

DB 240 QSGRGKADIMTYGTDGMRKIRDEGKAFEFYGANSNVIRKMGAFVLYLYEIKKY 296

RESULT 14
 ID AA001198 standard; Protein; 297 AA.

AC AAU01198;

DT 07-SEP-2001 (first entry)

DE Human adenine nucleotide translocator-1 (ANT-1) protein.

XX Human; adenine nucleotide translocator-1; ANT-1; MPT; cyclophilin;

KW mitochondrial permeability transition pore component; cell survival;

KW mitochondrial core component; mitochondrial related disorder; cancer;

XX Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

OS Homo sapiens.

PN WO200132876-A2.

PD 10-MAY-2001.

PF 03-NOV-2000; 2000WO-US30535.

PR 03-NOV-1999; 99US-0434354.

XX (MITO-) MITOKOR.

XX Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Fritger LG;

PI Vellicelabi G, Davis RE;

DR MPI: 2001-291054/30.

DR N-PSDB; AAS05901.

XX New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule

XX Disclosure; Fig 2; 186pp; English.

XX The present sequence represents human adenine nucleotide translocator-1
 CC (ANT-1) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.

XX Sequence 297 AA;

Query Match 89.9%; Score 1391.5; DB 22; Length 297;
 Best Local Similarity 88.6%; Pred. No. 5.5e-138;

Matches 263: Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTDALSFADFLAGVAAAIKSTAVAPIERVKLLLOVHASKOITADKOYKGIIDCVR 60
 Db 1 MGDHMSFLDKFLAGVAAAVSKTAVAPIERVKLLLOVHASKOISAEKQYKGIIDCVR 60

QY 61 IPKQEVLSFRKGLAVIRFPPTQALNFAFKDKYKQIFLGVDKRFQFRRYFAGNLASG 120
 Db 61 IPKQEVLSFRKGLAVIRFPPTQALNFAFKDKYKQIFLGVDKRFQFRRYFAGNLASG 120

QY 121 GAAGATSLCFEYPLDFARTRLADVDGKAGAREFERGLGDLVKIKYKSDGIRGLYQGFNV 180
 Db 121 GAAGATSLCFEYPLDFARTRLADVDGRR-AQREPHGLGDCIIFKISDGLRGLYQGFNV 179

QY 181 VQGIITIRAAVFGIYDTAKGMLPDPKNTHTVISMIAQVYAVAGLTSYFEDVYRRMM 240
 Db 180 VQGIITIRAAVFGIYDTAKGMLPDPKNTHTVISMIAQVYAVAGLTSYFEDVYRRMM 239

QY 241 QSGRKGIDIMYTGILDCMKRIARDEGKAFKFGKMSVNLGKMGAFVLVYDEIKKY 297
 Db 240 QSGRKGIDIMYTGILDCMKRIARDEGKAFKFGKMSVNLGKMGAFVLVYDEIKKY 296

RESULT 15

AAU10378

ID AAU10378 standard; Protein: 297 AA.

AC AAU10378;

DT 14-FEB-2002 (first entry)

DE Human adenine nucleotide translocator 1 (ANT1).

KW Human; adenine nucleotide translocator; ANT;

KM mitochondrial matrix protein.

OS Homo sapiens.

PN W0200185944-A2.

PD 15-NOV-2001.

PE 11-MAY-2001; 2001MO-US15416.

PR 11-MAY-2000; 2000US-0569327.

XX (MITO-) MITOKOR.

PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;

PI Ghosh SS, Moos WH, Fel Y, Carroll AK;

XX WPI; 2002-055598/07.

DR N-PSDB; AAS16688.

PT Novel recombinant expression construct for producing adenine nucleotide

PT translocator polypeptides; comprises a regulated promoter linked to

XX nucleic acid encoding the polypeptide

PS Claim 44; Fig 2; 147pp; English;

XX The invention relates to a recombinant expression construct (I)

CC comprising a regulated promoter operably linked to a nucleic acid

CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT

CC proteins mediate the exchange of ATP synthesised in the mitochondrial

CC matrix for ADP in the cytosol. (I) is useful for producing recombinant

CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and

CC culturing the host cell. (I) is also useful for targeting a polypeptide

CC of interest to a mitochondrial membrane, where ANT polypeptide is

CC expressed as a fusion protein with the polypeptide of interest.

CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is

CC useful for identifying an agent that binds to an ANT polypeptide. ANT

CC ligand is useful for determining the presence of an ANT polypeptide,

CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating

CC ANT from a biological sample, where the ANT ligand is covalently or non-

CC covalently bound to a solid phase. Detectably labeled ANT ligand is also

CC useful for identifying an agent that interacts with an ANT polypeptide.

CC The present sequence represents the amino acid sequence of human ANT1.

XX

SQ Sequence 297 AA;

Query Match 89.9%; Score 1391.5; DB 23; Length 297;

Best Local Similarity 88.6%; Pred. No. 5.5e-138;

Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTDALSFADFLAGVAAAIKSTAVAPIERVKLLLOVHASKOITADKOYKGIIDCVR 60
 Db 1 MGDHMSFLDKFLAGVAAAVSKTAVAPIERVKLLLOVHASKOISAEKQYKGIIDCVR 60

QY 61 IPKQEVLSFRKGLAVIRFPPTQALNFAFKDKYKQIFLGVDKRFQFRRYFAGNLASG 120
 Db 61 IPKQEVLSFRKGLAVIRFPPTQALNFAFKDKYKQIFLGVDKRFQFRRYFAGNLASG 120

QY 121 GAAGATSLCFEYPLDFARTRLADVDGKAGAREFERGLGDLVKIKYKSDGIRGLYQGFNV 180
 Db 121 GAAGATSLCFEYPLDFARTRLADVDGRR-AQREPHGLGDCIIFKISDGLRGLYQGFNV 179

QY 181 VQGIITIRAAVFGIYDTAKGMLPDPKNTHTVISMIAQVYAVAGLTSYFEDVYRRMM 240
 Db 180 VQGIITIRAAVFGIYDTAKGMLPDPKNTHTVISMIAQVYAVAGLTSYFEDVYRRMM 239

QY 241 QSGRKGIDIMYTGILDCMKRIARDEGKAFKFGKMSVNLGKMGAFVLVYDEIKKY 297
 Db 240 QSGRKGIDIMYTGILDCMKRIARDEGKAFKFGKMSVNLGKMGAFVLVYDEIKKY 296

Search completed: August 28, 2003, 19:38:48

Job time : 53.3919 secs

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OM protein - protein search, using SW model

Run on: August 28, 2003, 19:36:11 ; Search time 18.0202 Seconds
(without alignments)
699.696 Million cell updates/sec

Title: US-09-811-132-32

Perfect score: 1547

Sequence: 1 MTDALSPAKDFLAGVAAA.....LRGMGAFVLVYDEIKRYT 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCRTS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1547	100.0	298	4	US-09-434-354-48 Sequence 48, Appl
2	1454	94.0	298	4	US-09-434-354-49 Sequence 49, Appl
3	1411	91.2	298	3	US-08-961-871-10 Sequence 10, Appl
4	1391.5	89.9	297	4	US-09-434-354-47 Sequence 47, Appl
5	302	19.5	469	4	US-09-996-243-289 Sequence 289, App
6	301	19.5	469	3	US-09-188-930-339 Sequence 339, App
7	301	19.5	469	4	US-09-312-283C-339 Sequence 339, App
8	274	17.7	291	4	US-09-501-558-2 Sequence 2, Appl
9	274	17.7	335	4	US-09-482-273-118 Sequence 118, App
10	261.5	16.9	447	4	US-09-160-119-4 Sequence 4, Appl
11	261.5	16.9	674	4	US-09-160-119-2 Sequence 2, Appl
12	247	16.0	312	4	US-09-142-565-2 Sequence 2, Appl
13	244.5	15.8	311	2	US-08-775-009-33 Sequence 33, Appl
14	239.5	15.5	309	1	US-08-518-878B-51 Sequence 51, Appl
15	239.5	15.5	309	2	US-08-807-861A-51 Sequence 51, Appl
16	239.5	15.5	309	2	US-08-807-861A-51 Sequence 51, Appl
17	239.5	15.5	309	3	US-08-470-868A-51 Sequence 51, Appl
18	239.5	15.5	309	3	US-09-210-681-51 Sequence 51, Appl
19	239.5	15.5	309	4	US-08-946-719A-51 Sequence 51, Appl
20	236.5	15.3	299	1	US-08-547-983-51 Sequence 51, Appl
21	236.5	15.3	299	1	US-08-518-878B-56 Sequence 56, Appl
22	232.5	13.0	311	2	US-08-470-868A-56 Sequence 56, Appl
23	230.5	11.9	320	3	US-08-775-009-32 Sequence 32, Appl
24	230.5	11.9	320	3	US-08-933-750C-12 Sequence 12, Appl
25	227	14.7	308	2	US-09-234-613-12 Sequence 2, Appl
26	227	14.7	308	2	US-08-937-466-2 Sequence 2, Appl
27	227	14.7	308	3	US-09-172-528-2 Sequence 2, Appl
					US-09-318-199-6 Sequence 2, Appl

28	227	14.7	308	3	US-09-503-579-2	Sequence 2, Appl
29	223	14.4	432	2	US-08-937-466-4	Sequence 4, Appl
30	223	14.4	432	2	US-09-172-528-4	Sequence 4, Appl
31	223	14.4	432	3	US-09-318-199-4	Sequence 4, Appl
32	223	14.4	432	3	US-09-503-579-4	Sequence 4, Appl
33	219.5	14.2	293	4	US-09-501-558-4	Sequence 4, Appl
34	218.5	14.1	303	1	US-08-294-522B-36	Sequence 36, Appl
35	217.5	14.1	303	1	US-08-518-878B-37	Sequence 37, Appl
36	217.5	14.1	303	2	US-08-807-861A-37	Sequence 37, Appl
37	217.5	14.1	303	2	US-08-470-868A-37	Sequence 37, Appl
38	217.5	14.1	303	3	US-09-210-681-37	Sequence 37, Appl
39	217.5	14.1	303	3	US-08-946-719A-37	Sequence 37, Appl
40	217.5	14.1	303	4	US-09-547-983-37	Sequence 37, Appl
41	191	12.3	328	3	US-09-068-140A-15	Sequence 15, Appl
42	190.5	12.3	256	2	US-08-937-466-6	Sequence 6, Appl
43	190.5	12.3	256	2	US-09-172-528-6	Sequence 6, Appl
44	190.5	12.3	256	3	US-09-318-199-6	Sequence 6, Appl
45	190.5	12.3	256	3	US-09-503-579-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-434-354-48
Sequence 48, Application US/09434354

Patent No. 6562563

GENERAL INFORMATION:

APPLICANT: Murphy, Anne N.

APPLICANT: Clevenger, William

APPLICANT: Wiley, Sandra Elleen

APPLICANT: Andreyev, Alexander Y.

APPLICANT: Frigeri, Luciano G.

APPLICANT: Velicelab, Gonul

APPLICANT: Davis, Robert E.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING

TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR

TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS

FILE REFERENCE: 660088.433

CURRENT APPLICATION NUMBER: US/09/434,354

CURRENT FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 54

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 48

LENGTH: 298

TYPE: PRT

ORGANISM: Homo sapien

US-09-434-354-48

Query Match

Best Local Similarity 100.0%; Score 1547; DB 4; Length 298;

Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTDALSPAKDFLAGVAAAISKTAAPVPIERVKLLQVOHASKQITADQYKGIIDCVYR 60
DB	1	MTDALSPAKDFLAGVAAAISKTAAPVPIERVKLLQVOHASKQITADQYKGIIDCVYR 60
QY	61	IPEDQVLSFWGNLANVRIYPTQALNFAFDKQITGLGVDRKTOFWRRFAGMLASG 120
DB	61	IPEDQVLSFWGNLANVRIYPTQALNFAFDKQITGLGVDRKTOFWRRFAGMLASG 120
QY	121	GAAGATSLCFVYPLDFARTRLADYVKGAEERFGLDCLVITYKSDGKGLGYGFNYS 180
DB	121	GAAGATSLCFVYPLDFARTRLADYVKGAEERFGLDCLVITYKSDGKGLGYGFNYS 180
QY	181	VGGIIYRAAYGCIYDTAKGMLPDPKNTIIVISWMTAQVTVAVAGLTSVPEDTVRRMM 240
DB	181	VGGIIYRAAYGCIYDTAKGMLPDPKNTIIVISWMTAQVTVAVAGLTSVPEDTVRRMM 240
QY	241	OSGRKGTDMYGTGLDCMKRIARDEGKAFKFGAMSNVLRGMGAFVLVYDEIKRYT 298
DB	241	OSGRKGTDMYGTGLDCMKRIARDEGKAFKFGAMSNVLRGMGAFVLVYDEIKRYT 298

RESULT 2
US-09-434-354-49
Sequence 49, Application US/09434354
Patent No. 6562563
GENERAL INFORMATION:
APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigeri, Luciano G.
APPLICANT: Velicelbel, Gonul
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
FILE REFERENCE: 660088.433
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 49
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-434-354-49

Query Match 94.0%; Score 1454; DB 4; Length 298;
Best Local Similarity 92.6%; Pred. No. 6.3e-159;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTDALSFADFLAGVAAIASTAVAPIERVKLLLOVHASQITADKOYKGIIDCVR 60
DB 1 MTDALSFADFLAGVAAIASTAVAPIERVKLLLOVHASQITADKOYKGIIDCVR 60
QY 61 IPKEQVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRTQFRYFAGNLSG 120
DB 61 IPKEQVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRTQFRYFAGNLSG 120
QY 121 GAAGATSLCEVYPLDFARTLADVKGAEERERGLDGLVTKSDGIRGLYQGSVS 180
DB 121 GAAGATSLCEVYPLDFARTLADVKGAEERERGLDGLVTKSDGIRGLYQGSVS 180
QY 181 VOGIIIRAAVFGYIDPAKMLPDPKNTHTVISMTAQTYTAAVAGLSTYFDDVRRMM 240
DB 181 VOGIIIRAAVFGYIDPAKMLPDPKNTHTVISMTAQTYTAAVAGLSTYFDDVRRMM 240
QY 241 QSGRKGTDIMYTGTLDCMRKIARDEGKAFKFGAMSNTVLRMGAGAFVLYIDEIKK 296
DB 241 QSGRKGTDIMYTGTLDCMRKIARDEGKAFKFGAMSNTVLRMGAGAFVLYIDEIKK 296

RESULT 3
US-08-961-871-10
Sequence 10, Application US/08961871
Patent No. 6013858
GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigeri, Luciano G.
APPLICANT: Velicelbel, Gonul
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
FILE REFERENCE: 660088.433
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Perber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-871-10

Query Match 91.2%; Score 1411; DB 3; Length 298;
Best Local Similarity 89.2%; Pred. No. 5.6e-154;
Matches 265; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 1 MTDALSFADFLAGVAAIASTAVAPIERVKLLLOVHASQITADKOYKGIIDCVR 60
DB 1 MTDALSFADFLAGVAAIASTAVAPIERVKLLLOVHASQITADKOYKGIIDCVR 60
QY 61 IPKEQVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRTQFRYFAGNLSG 120
DB 61 IPKEQVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRTQFRYFAGNLSG 120
QY 121 GAAGATSLCEVYPLDFARTLADVKGAEERERGLDGLVTKSDGIRGLYQGSVS 180
DB 121 GAAGATSLCEVYPLDFARTLADVKGAEERERGLDGLVTKSDGIRGLYQGSVS 180
QY 181 VOGIIIRAAVFGYIDPAKMLPDPKNTHTVISMTAQTYTAAVAGLSTYFDDVRRMM 240
DB 181 VOGIIIRAAVFGYIDPAKMLPDPKNTHTVISMTAQTYTAAVAGLSTYFDDVRRMM 240
QY 241 QSGRKGTDIMYTGTLDCMRKIARDEGKAFKFGAMSNTVLRMGAGAFVLYIDEIKK 297
DB 241 QSGRKGTDIMYTGTLDCMRKIARDEGKAFKFGAMSNTVLRMGAGAFVLYIDEIKK 297

RESULT 4
US-09-434-354-47
Sequence 47, Application US/09434354
Patent No. 6562563
GENERAL INFORMATION:
APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigeri, Luciano G.
APPLICANT: Velicelbel, Gonul
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
FILE REFERENCE: 660088.433
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 47
LENGTH: 297
TYPE: PRT
ORGANISM: Homo sapien

US-09-434-354-47

Query Match 89.9%; Score 1391.5; DB 4; Length 297;
 Best Local Similarity 88.6%; Pred. No. 9,8e-152;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTDAALFAPDDELGLAGVAAAIKTAAPVAPTEVKKLLLOVHASKITADKOTKGIIDCVR 60
 1 MGDAMSFELKDFLGAVAASVKTAVAPTEVKKLLLOVHASKITADKOTKGIIDCVR 60
 QY 61 IPKOEVLSPFMRGLANVIREPTQALNFARKDKYKQTEFGGVKROFMFEPFAGNLSG 120
 61 IPKOEVLSPFMRGLANVIREPTQALNFARKDKYKQTEFGGVKROFMFEPFAGNLSG 120
 QY 121 GAAGATSLCEFYPPDFAFRTLAADVGRKAGAEFEGGLDGLVKKYKSDIGLXOGFVNS 180
 121 GAAGATSLCEFYPPDFAFRTLAADVGRKAGAEFEGGLDGLVKKYKSDIGLXOGFVNS 179
 Db 180 VQGIITRAAFEGYDFAKGMPLDPKNTHTVISMIAQTVTAVALGASYPEDTVRRMM 240
 180 VQGIITRAAFEGYDFAKGMPLDPKNTHTVISMIAQTVTAVALGASYPEDTVRRMM 239
 QY 241 QSGRRKGDIMTGLDCKRKARDEGKAFKFGAMSNTLRMGAFVLYLDEIKKY 297
 241 QSGRRKGDIMTGLDCKRKARDEGKAFKFGAMSNTLRMGAFVLYLDEIKKY 296
 Db 240 QSGRRKGDIMTGLDCKRKARDEGKAFKFGAMSNTLRMGAFVLYLDEIKKY 296

RESULT 5

US-09-996-243-289

Sequence 289, Application US/09996243
 Patent No. 6478825

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2730P1C13
 CURRENT APPLICATION NUMBER: US/09/996,243
 PRIOR FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/087106
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087609
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087759
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087827
 PRIOR FILING DATE: 1998-06-03
 PRIOR APPLICATION NUMBER: 60/088021
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088025
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088026
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088028
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088029
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088030
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088033
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088326
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088167
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088202
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088212
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088217
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088655
 PRIOR FILING DATE: 1998-06-09
 PRIOR APPLICATION NUMBER: 60/088734
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088738
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088742
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088810
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088824
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088826
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088858
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088861
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088876
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/089105
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089440
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089512
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089514
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089532
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089538
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089598


```

DB 293 IAOSITVMEVLTNRMA--LRKTG---OYSGMLDCARILLAKEGVAAYKYIIPMLGII 347
OY 186 IYRAAFGIYDPANGMLDPKNTHT-----VISMIAQTVTAAG-LTSYPPDT 233
DB 348 PYAGIDLAIVETL-----KNTWLOQRYAVNSADGCVVLLACGSISSCGGLASYPPLAL 400
OY 234 VRRMMQSGRKGTIDIMYTGILDCWRKIARDEGKAFKGMASVNLKMGAFV-LVLYD 292
DB 401 VRTMQOASIEGAEPTVMSSL--FKQILRTGAGFLYRGLAPNPMKVIAPAVISISYVYE 458
OY 293 EIK 295
DB 459 NLK 461

```

RESULT 7

```

US-09-312-283C-339
; Sequence 339, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Orlust, Rene
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-339

```

Query Match 19.5%; Score 301; DB 4; Length 469;

Best Local Similarity 28.4%; Pred. No. 7e-26; Matches 86; Conservative 62; Mismatches 109; Indels 46; Gaps 12;

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OY 10 KDLAAGVAAAIKSTAVAPIERVKLLLOVHASQKITADKQYKGIIDCV---RIPKEO 65
DB 188 RHLVAGGAGAVSRCTAPDLRLKVLQV--HASSNNM-----CIVGSGTMINRG 237
OY 66 EVLSWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRRYRAGNLASGGAAGA 125
DB 238 GAKSLMRNGINVLKIAPESAIKFMAYQMKR--LVGSDQET--LRHERLVAGSLAGA 292
OY 126 TSLCFVYPLDFARFRLADVKGAREFRGLDCLVYIKSDGKIGLYOGFNVVOGII 185
DB 293 IAOSITVMEVLTNRMA--LRKTG---OYSGMLDCARILLAKEGVAAYKYIIPMLGII 347
OY 186 IYRAAFGIYDPANGMLDPKNTHT-----VISMIAQTVTAAG-LTSYPPDT 233
DB 348 PYAGIDLAIVETL-----KNTWLOQRYAVNSADGCVVLLACGSISSCGGLASYPPLAL 400
OY 234 VRRMMQSGRKGTIDIMYTGILDCWRKIARDEGKAFKGMASVNLKMGAFV-LVLYD 292
DB 401 VRTMQOASIEGAEPTVMSSL--FKQILRTGAGFLYRGLAPNPMKVIAPAVISISYVYE 458
OY 293 EIK 295
DB 459 NLK 461

```

RESULT 8

```

US-09-501-558-2
; Sequence 2, Application US/09501558
; Patent No. 6403784
; GENERAL INFORMATION:

```

```

; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur E.
; TITLE OF INVENTION: No. 6403784e1 Human Uncoupling Proteins and
; FILE REFERENCE: Lex-0012-USA
; CURRENT APPLICATION NUMBER: US/09/501,558
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-501-558-2

```

Query Match 17.7%; Score 274; DB 4; Length 291;

Best Local Similarity 27.8%; Pred. No. 4.3e-23; Matches 85; Conservative 55; Mismatches 134; Indels 32; Gaps 9;

```

OY 4 AALSAKDFLAGGVAAAIKSTAVAPIERVKLLLOVHAS-----KQITADKQYKGIIDCV 58
DB 2 SALNM--KRPVYGGIASTAECGTFPIDLTKTRIQIGOTNDKKEFI---RYKMLHAL 56
OY 59 VAIRPEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRRYRAGNL 118
DB 57 VAIRGEQKALYSIAPMLAQASYGTIKIGYSIKRFLEREDF-----LPINVI 111
OY 119 SCGAAGNSLCLFVYPLDFARFRLADVKGAREFRGLDCLVYIKSDGKIGLYOGFN 178
DB 112 CGLISGVISSTIANPTDVLKIRMQOASNTIQG-----CGWGNFMNINYOQEGTGRGLKGV 166
OY 179 VSVQGIITRYAFEGYDPAK-----GMLDPKNTHTYISMIAQTVTAAGLTSYPPD 232
DB 167 LTAORAIVGVGLPYDIDTKKHLILSGMLGYTHYHLSF---TCGLAALASNPVD 222
OY 233 TVRRMMQSG--RKGTIDIMYTGILDCWRKIARDEGKAFKGMASVNLK--GNGAFVLYL 290
DB 223 VRTMQOASIEGAEPTVMSSL--FKQILRTGAGFLYRGLAPNPMKVIAPAVISISYV 282
OY 291 YDEIKK 296
DB 283 YQLKK 288

```

RESULT 9

```

US-09-482-273-118
; Sequence 118, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P1
; CURRENT APPLICATION NUMBER: US/09/482,273
; EARLIER FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1998-07-14
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (335)

```


SEQ ID NO 2
LENGTH: 312
TYPE: PRT
ORGANISM: HOMO SAPIEN
US-09-142-565-2

Query Match 16.0%; Score 247; DB 3; Length 312;
Best Local Similarity 24.8%; Pred. No. 6.2e-20;
Matches 76; Conservative 56; Mismatches 149; Indels 26; Gaps 8;

QY 2 TDAALSKAPDLACGAAATSKTAVAPIERVKLLQVQHASKOTLADK--QYKGLIOCV 59
DB 7 SDVPTAAVFKLGGTACFADLTFTPLDTAKRLQIOGENQAQVTAALVYRGVLTLL 66
QY 60 RIRPEQELSEFWRGNLANVIRFPTQALNFAFKDKYKQIFL--GGVDKRTQFWRFGNLA 118
DB 67 TMVTEPCSPSYNGLVAGLQMSFASIRIGLYDSVQVYPPKADNSLTLTLLA----- 122
QY 119 SGGAAGATSLCFYPLDPARFLAADV--GKAGAEERERGLGDLVKIKSDGKGLYQG 176
DB 123 -GCTTGMAAVYCAQPTDVVKVRFOASIHLPSSRSDKXSGTMDAYRTIAREEGVYGLMKG 181
QY 177 FNVSVGIIYRAVYFGIDYFAK-----GMLPDPKNTHIYSMMIAQVTAVALGTSYP 230
DB 182 TLPIMRNATVNCLEVVYTYDILKEKLDYHLTDNFPCHFSAGAGFCATVVAS---P 237
QY 231 FDIYRRMMQSGRRKGTDMYTGTLDGWRKIARDEGKAFPKGAMSNVLR--GMGAFVLV 289
DB 238 VDVKRTVYM-----NSPPGQYFSPLDGKIMKVAQEGPAFYKGTPTPSRLGSMNVVAFV 292
QY 290 LYDEIKR 296
DB 293 TYEQILKR 299

RESULT 13

US-08-775-009-33
Sequence 33, Application US/08775009
Patent No. 5935783

GENERAL INFORMATION:
APPLICANT: Gong, Wellong
APPLICANT: Emanuel, Beverly S.
APPLICANT: Budart, Marcia L.
TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digestion and
TITLE OF INVENTION: Velocardiofacial Syndrome Minimal Critical Region
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESS: No. 5935783is, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/775, 009
FILING DATE: 27-DEC-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yalko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CH-0681
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:

LENGTH: 311 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-775-009-33

Query Match 15.8%; Score 244.5; DB 2; Length 311;
Best Local Similarity 28.1%; Pred. No. 1.2e-19;
Matches 83; Conservative 47; Mismatches 138; Indels 27; Gaps 8;

QY 10 KDLFAGVAAIASTAVAPIERVKLLQVQHASKOTLADKQYKGLIQCVRIRPEQELVS 69
DB 27 KAILAGGIAGIEICITPTEYVKTOQLDERAN---PPRYRGIGDVRQIVSHGYLG 82
QY 70 FWRGNLANVIRFPTQALNFA---FKDKYKQIFLGVDKRTQFWRFGNLANSGAAGAT 126
DB 83 LYRGLSSLLYSIPKAAVRFQMEFLSNHMDAQGRDLSR-----RGLLGAGVAAE 135
QY 127 SLCEFYPLDPARFLAADVGRKAGAEERERGLGDLVKIKSDGKGLYQGFNVSVQIGII 186
DB 136 AVVVYCPMEYKVKRTHD--QTSSNPKYRGFPFHGREIVREGGLKGTVOGLATATYLGGS 193
QY 187 YRAVFGIYDPAKGMLEPPKNTHIYSMMIAQVTAVALGTSY----PDTVRRMMQOS 242
DB 194 NQAIRFEYMTSLRMY--OGDNPNKPMNPLITGVFGAVAGAAVSFGNTPLVDYIKTRMGL 252
QY 243 GRKGTDMYTGTLDGWRKIARDEGKAFPKGAMSNVLR--GMGAFVLVLYDEIKR 296
DB 253 AHR-----YRNTLDGVOILKNEGKAFYKGTVPRLGVNCDVALFVYIDEVVR 302

RESULT 14

US-08-518-878B-51
Sequence 51, Application US/08518878B
Patent No. 5702902

GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518, 878B
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-518-878B-51

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 19:38:56 ; Search time 19.355 Seconds

(without alignments)
2105.969 Million cell updates/sec

Title: US-09-811-132-32

Perfect score: 1547
Sequence: 1 MTDALSPAKDFLAGVAA.....LRGMGAFLVLYDEIKRYT 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 510680 seqs, 136781880 residues

Total number of hits satisfying chosen parameters: 510680

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

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18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1547	100.0	298	9	US-09-811-094-32
2	1547	100.0	298	9	US-09-810-644-32
3	1547	100.0	298	10	US-09-185-904A-32
4	1454	94.0	298	9	US-09-811-094-33
5	1454	94.0	298	9	US-09-810-644-33
6	1454	94.0	298	10	US-09-185-904A-33
7	1391.5	89.9	297	9	US-09-811-094-31
8	1391.5	89.9	297	9	US-09-810-644-31
9	1391.5	89.9	297	10	US-09-185-904A-31
10	752.5	48.6	318	10	US-09-801-368-252
11	741.5	47.9	381	12	US-10-141-478A-2
12	741.5	47.9	386	9	US-09-734-569-170
13	734	47.4	308	15	US-10-128-714-3338
14	734	47.4	308	15	US-10-128-714-8338
15	677.5	43.8	677	12	US-10-259-165-192

16	484	31.3	132	9	US-09-925-301-1459	Sequence 1459, App
17	448	29.0	87	9	US-09-864-761-36440	Sequence 36440, A
18	351	22.7	477	10	US-09-777-921A-2	Sequence 2, App11
19	350	22.6	475	10	US-09-777-921A-4	Sequence 4, App11
20	323.5	20.9	410	10	US-09-777-921A-5	Sequence 5, App11
21	302	19.5	469	9	US-09-989-722-289	Sequence 289, App
22	302	19.5	469	9	US-09-989-723-289	Sequence 289, App
23	302	19.5	469	9	US-09-989-279-289	Sequence 289, App
24	302	19.5	469	9	US-09-989-731-289	Sequence 289, App
25	302	19.5	469	10	US-09-989-732-289	Sequence 289, App
26	302	19.5	469	10	US-09-989-732-289	Sequence 289, App
27	302	19.5	469	10	US-09-981-073-289	Sequence 289, App
28	302	19.5	469	10	US-09-990-442-289	Sequence 289, App
29	302	19.5	469	10	US-09-991-163-289	Sequence 289, App
30	302	19.5	469	10	US-09-993-604-289	Sequence 289, App
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32	302	19.5	469	10	US-09-990-444-289	Sequence 289, App
33	302	19.5	469	10	US-09-989-721-289	Sequence 289, App
34	302	19.5	469	10	US-09-989-735-289	Sequence 289, App
35	302	19.5	469	10	US-09-989-735-289	Sequence 289, App
36	302	19.5	469	10	US-09-990-444-289	Sequence 289, App
37	302	19.5	469	10	US-09-991-181-289	Sequence 289, App
38	302	19.5	469	10	US-09-989-730-289	Sequence 289, App
39	302	19.5	469	10	US-09-990-436-289	Sequence 289, App
40	302	19.5	469	10	US-09-993-687-289	Sequence 289, App
41	302	19.5	469	11	US-09-989-734-289	Sequence 289, App
42	302	19.5	469	11	US-09-997-653-289	Sequence 289, App
43	302	19.5	469	11	US-09-993-667-289	Sequence 289, App
44	302	19.5	469	11	US-09-997-628-289	Sequence 289, App
45	302	19.5	469	11	US-09-997-666-289	Sequence 289, App

ALIGNMENTS

RESULT 1
US-09-811-094-32
; Sequence 32, Application US/09811094
; Patent No. US20010044144A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willet, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yachong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420DA
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-811-094-32

Query Match 100.0%; Score 1547; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.2e-159;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MTDALSPAKDFLAGVAAISKTAVADIERVKLLQVHASKOITADKQKGIIDCVR 60
QY 61 IPKQEVLSFRGNANIRYFPQALNFARFDKTKQIFLGGVDRKQFQFVFNAGNLASG 120
DB 61 IPKQEVLSFRGNANIRYFPQALNFARFDKTKQIFLGGVDRKQFQFVFNAGNLASG 120

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        |||||||
DB      121 GAAGTSTLCFYPLDPFATRLAADVGKGAEEFGGLDCLVTKIKSGIKLGYGFNVS 180
OY      161 VGGIIITRAAAYFGIYDTAKGMLPDKPNTHIVISMMIAOTVTAAVAGLTSPEDTVRRMMM 240
        |||||||
DB      161 VGGIIITRAAAYFGIYDTAKGMLPDKPNTHIVISMMIAOTVTAAVAGLTSPEDTVRRMMM 240
OY      241 QSGRKGTDIMYTGTLDCKWRKIARDEGKAFFKGAMSNLRGMGAFVLVLYDEIKKYT 298
        |||||||
DB      241 QSGRKGTDIMYTGTLDCKWRKIARDEGKAFFKGAMSNLRGMGAFVLVLYDEIKKYT 298

RESULT 2
US-09-810-644-32
; Sequence 32, Application US/09810644
; Patent No. US20020012992A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yezhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
FILE REFERENCE: 660088.420D3
CURRENT APPLICATION NUMBER: US/09/810.644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-810-644-32

Query Match          100.0%; Score 1547; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 4,2e-159;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 MTDAALSAFAKFLAGVAAAISTKAVAPIERVKLLQVOHASKOTTADKOYGIIDCYVR 60
OY      61 IPKEDEVLSFWRGMLANYIRYPTQALNFAEKDKYQJIFLGVDKRTQFMRYFAGNLASG 120
DB      61 IPKEDEVLSFWRGMLANYIRYPTQALNFAEKDKYQJIFLGVDKRTQFMRYFAGNLASG 120
OY      121 GAAGTSTLCFYPLDPFATRLAADVGKGAEREFGGLDCLVTKIKSGIGLGYGFNVS 180
DB      121 GAAGTSTLCFYPLDPFATRLAADVGKGAEREFGGLDCLVTKIKSGIGLGYGFNVS 180
OY      161 VGGIIITRAAAYFGIYDTAKGMLPDKPNTHIVISMMIAOTVTAAVAGLTSPEDTVRRMMM 240
DB      161 VGGIIITRAAAYFGIYDTAKGMLPDKPNTHIVISMMIAOTVTAAVAGLTSPEDTVRRMMM 240
OY      241 QSGRKGTDIMYTGTLDCKWRKIARDEGKAFFKGAMSNLRGMGAFVLVLYDEIKKYT 298
DB      241 QSGRKGTDIMYTGTLDCKWRKIARDEGKAFFKGAMSNLRGMGAFVLVLYDEIKKYT 298

RESULT 3
US-09-185-904A-32
; Sequence 32, Application US/09185904A
; Patent No. US20020177185A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
```

```

; APPLICANT: Clevenger, William
; APPLICANT: Willey, Sandra Eileen
; APPLICANT: Willey, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
; TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420
; CURRENT APPLICATION NUMBER: US/09/185,904A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-185-904A-32

Query Match      100.0%; Score 1547; DB 10; Length 298;
Best Local Similarity 100.0%; Pred. No. 4,2e-159;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-811-094-33

; APPLICANT: Clevenger, William
; APPLICANT: Willey, Sandra Eileen
; APPLICANT: Willey, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yezhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-33

Query Match      94.0%; Score 1454; DB 9; Length 298;
Best Local Similarity 92.6%; Pred. No. 4,9e-149;

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Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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Db 1 MTEQAIKSPAKDFLAGGIAAISKTAAPIERVKLLQVHASKQITADKQKGIIDCYVR 60
OY 61 IPKEQVLSFWKGNLANIYRFPQALNFAFKDKYKQJFLGVDKRTQFWRYFAGNLSG 120
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Db 61 IPKEQVLSFWKGNLANIYRFPQALNFAFKDKYKQJFLGVDKRTQFWRYFAGNLSG 120
OY 121 GAAGATSLCFYPLDFARTRLAADVGKAGAREFRGLDCLVKIKSDIGIKLYOGFVNS 180
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Db 121 GAAGATSLCFYPLDFARTRLAADVGKAGAREFRGLDCLVKIKSDIGIKLYOGFVNS 180
OY 181 VOGIIIRAAAFGYIDTAKGMLPDPKNTIYISMMIAOTVAVAGLTSYPTDVARRRMM 240
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 VOGIIIRAAAFGYIDTAKGMLPDPKNTIYISMMIAOTVAVAGVSTPDTVARRRMM 240
OY 241 QSGRKGTDIMYTGTLDCWKRKIADEGKAFKGAWSNVLKMGAFVLYLDEIRK 296
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 QSGRKGADIMYTGTVDCWKRKIFRDEGKAFKGAWSNVLKMGAFVLYLDEIRK 296
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RESULT 5

US-09-810-644-33
Sequence 33, Application US/09810644
Patent No. US20020012992A1

GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-810-644-33

Query Match 94.0%; Score 1454; DB 9; Length 298;
Best Local Similarity 92.6%; Pred. No. 4.9e-149;

Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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Db 1 MTEQAIKSPAKDFLAGGIAAISKTAAPIERVKLLQVHASKQITADKQKGIIDCYVR 60
OY 61 IPKEQVLSFWKGNLANIYRFPQALNFAFKDKYKQJFLGVDKRTQFWRYFAGNLSG 120
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 IPKEQVLSFWKGNLANIYRFPQALNFAFKDKYKQJFLGVDKRTQFWRYFAGNLSG 120
OY 121 GAAGATSLCFYPLDFARTRLAADVGKAGAREFRGLDCLVKIKSDIGIKLYOGFVNS 180
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GAAGATSLCFYPLDFARTRLAADVGKAGAREFRGLDCLVKIKSDIGIKLYOGFVNS 180
OY 181 VOGIIIRAAAFGYIDTAKGMLPDPKNTIYISMMIAOTVAVAGLTSYPTDVARRRMM 240
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 VOGIIIRAAAFGYIDTAKGMLPDPKNTIYISMMIAOTVAVAGVSTPDTVARRRMM 240
OY 241 QSGRKGTDIMYTGTLDCWKRKIADEGKAFKGAWSNVLKMGAFVLYLDEIRK 296
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 QSGRKGADIMYTGTVDCWKRKIFRDEGKAFKGAWSNVLKMGAFVLYLDEIRK 296
```

RESULT 6

US-09-185-904A-33
Sequence 33, Application US/09185904A
Patent No. US20020177185A1

GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-185-904A-33

Query Match 94.0%; Score 1454; DB 10; Length 298;
Best Local Similarity 92.6%; Pred. No. 4.9e-149;

Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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OY 1 MTDALSFADFLAGVAAAIKTAAPIERVKLLQVHASKQITADKQKGIIDCYVR 60
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Db 1 MTEQAIKSPAKDFLAGGIAAISKTAAPIERVKLLQVHASKQITADKQKGIIDCYVR 60
OY 61 IPKEQVLSFWKGNLANIYRFPQALNFAFKDKYKQJFLGVDKRTQFWRYFAGNLSG 120
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Db 61 IPKEQVLSFWKGNLANIYRFPQALNFAFKDKYKQJFLGVDKRTQFWRYFAGNLSG 120
OY 121 GAAGATSLCFYPLDFARTRLAADVGKAGAREFRGLDCLVKIKSDIGIKLYOGFVNS 180
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GAAGATSLCFYPLDFARTRLAADVGKAGAREFRGLDCLVKIKSDIGIKLYOGFVNS 180
OY 181 VOGIIIRAAAFGYIDTAKGMLPDPKNTIYISMMIAOTVAVAGLTSYPTDVARRRMM 240
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 VOGIIIRAAAFGYIDTAKGMLPDPKNTIYISMMIAOTVAVAGVSTPDTVARRRMM 240
OY 241 QSGRKGTDIMYTGTLDCWKRKIADEGKAFKGAWSNVLKMGAFVLYLDEIRK 296
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Db 241 QSGRKGADIMYTGTVDCWKRKIFRDEGKAFKGAWSNVLKMGAFVLYLDEIRK 296
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RESULT 7

US-09-811-094-31
Sequence 31, Application US/09811094
Patent No. US2001004414A1

GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37

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: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 31
: LENGTH: 297
: TYPE: PRT
: ORGANISM: Homo sapien
US-09-811-094-31

```

Query Match	89.98;	Score 1391.5;	DB 9;	Length 297;
Best Local Similarity	88.68;	Pred. NO. 2.9e-142;		
Matches 263; Conservative	17;	Mismatches 16;	Indels 1;	Gaps 1

QY 1 MTPAALSEFKDFLAGGVAALISKAAVAPPIERVKLLQVOHASKQTADKRYKKGIIDCVRR 60
DB 1 MGDAWMSFLKDLTAGAVAAAVSKRAVAPIERVKLLQVOHASKQSIAEKRYKKGIIDCVRR 60

0y 61 IPKQGVLSFWRGMLANVIRYFPQALNFAFKDKKQIFLGSGVDVDRTOEKNRYFAGSLASG 120
 0y 61 IPKQGVLSFWRGMLANVIRYFPQALNFAFKDKKQIFLGSGVDVDRTOEKNRYFAGSLASG 120
 Db 61 IPKQGVLSFWRGMLANVIRYFPQALNFAFKDKKQIFLGSGVDVDRTOEKNRYFAGSLASG 120

121 GAAGATGCTCCTVPLDFAKTRLAADVGR - AOREEFGIGDCIIKPKSDGIRGLYOGFNVS 179
 .
 121 GAAGATGCTCCTVPLDFAKTRLAADVGRKREERGLGDLVKIKYKSDGIRGLYOGFNVS 180
 121 GAAGATGCTCCTVPLDFAKTRLAADVGRKREERGLGDLVKIKYKSDGIRGLYOGFNVS 181
 121 GAAGATGCTCCTVPLDFAKTRLAADVGRKREERGLGDLVKIKYKSDGIRGLYOGFNVS 182
 121 GAAGATGCTCCTVPLDFAKTRLAADVGRKREERGLGDLVKIKYKSDGIRGLYOGFNVS 183
 121 GAAGATGCTCCTVPLDFAKTRLAADVGRKREERGLGDLVKIKYKSDGIRGLYOGFNVS 184
 121 GAAGATGCTCCTVPLDFAKTRLAADVGRKREERGLGDLVKIKYKSDGIRGLYOGFNVS 185
 121 GAAGATGCTCCTVPLDFAKTRLAADVGRKREERGLGDLVKIKYKSDGIRGLYOGFNVS 186
 121 GAAGATGCTCCTVPLDFAKTRLAADVGRKREERGLGDLVKIKYKSDGIRGLYOGFNVS 187
 121 GAAGATGCTCCTVPLDFAKTRLAADVGRKREERGLGDLVKIKYKSDGIRGLYOGFNVS 188
 121 GAAGATGCTCCTVPLDFAKTRLAADVGRKREERGLGDLVKIKYKSDGIRGLYOGFNVS 189
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 121 GAAGATGCTCCTVPLDFAKTRLAADVGRKREERGLGDLVKIKYKSDGIRGLYOGFNVS 192
 121 GAAGATGCTCCTVPLDFAKTRLAADVGRKREERGLGDLVKIKYKSDGIRGLYOGFNVS 193
 121 GAAGATGCTCCTVPLDFAKTRLAADVGRKREERGLGDLVKIKYKSDGIRGLYOGFNVS 194
 121 GAAGATGCTCCTVPLDFAKTRLAADVGRKREERGLGDLVKIKYKSDGIRGLYOGFNVS 195
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 121 GAAGATGCTCCTVPLDFAKTRLAADVGRKREERGLGDLVKIKYKSDGIRGLYOGFNVS 197
 121 GAAGATGCTCCTVPLDFAKTRLAADVGRKREERGLGDLVKIKYKSDGIRGLYOGFNVS 198
 121 GAAGATGCTCCTVPLDFAKTRLAADVGRKREERGLGDLVKIKYKSDGIRGLYOGFNVS 199
 121 GAAGATGCTCCTVPLDFAKTRLAADVGRKREERGLGDLVKIKYKSDGIRGLYOGFNVS 200

Db

180 VGGIIIRAYFGYYDTAKGMLPDKNVHIFVSNMIAQSYATAVAGLLSTPEFDIVRRRM 239

240 QSGHKGADIMYTGTVDCWRKRIAKDEGAKAFKGMASNVLRGMGGFAVLVLDEIRKY 296

RESULT 8
US-09-810-644-31
; Sequence 31, Application US/09810644

```

: GENERAL INFORMATION:
: APPLICANT: Anderson, Christen M.
: APPLICANT: Davis, Robert E.

```

: APPLICANT: Willey, Sandra Eileen
: APPLICANT: Miller, Scott W.
: APPLICANT: Szabo, Tomas R.

: APPLICANT: MOOS, Walter H.
 : APPLICANT: Pel, Yezhong
 : TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
 : PART OF INVENTION:

```

:
:
: FILE REFERENCE: 660088.420D3
:
: CURRENT APPLICATION NUMBER: US/09/810,644
:
: CURRENT FILING DATE: 2001-03-14
:
: NUMBER OF SEQ. ID NOS.: 37
:

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: SOFTWARE: FASTSEO  IoT Windows Version 3.0
: SEO ID NO 31
: LENGTH: 297
: TYPE: PRT

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ORGANISM:ROMO sapien	
US-09-810-644-31	
Query Match	89.9%: Score 1391.5: DB 9: Length 297:

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1 MEDAALSEAKDFLAGGVAAAISKTAAPAPPIERVKLLLOVOHASKOTITADROYKGIIDCVVR 60
2                                     Mismatches 1; Gaps 1.
3
4 best: b0cd4331a1a1c4c 60.0%; File: NO. 2.3c.14;
5 Matches 263; Conservative 17; Mismatches 16;
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Db 1 MGHAMSELTDFLAGVAAPAAVAPIERVKLLQVHASKQJSAEKYKGIIIDCVR 60
61 IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIEFGVDKRTQEFRRYFAGNLASG 120

121 GAAGATSLCFVYPDLDFARTRLADVKGAGAEERERGLGDLVKKIKKSDGKIGLYOGFNVS 180
121 1PEQGFSLFWKGNLANVYTRFPFOALNFAFKDKYIKQLFSGVDVHHKQFRRYFAGNLASC 120

.....

Db 121 GAAGATSLCEVYPDLDFAPTRLAADYGR - AQEHEFLGDCIIKIKFSKGLNGLYQGFVNS 179

QY 181 VQGIITTYRAAYGIVDTAKGMLPDEKRNHIVLSMIAQTVYAVAGLISYPRDYTRRRRRMM 244

Db 180 VQGIITTYRAAYGIVDTAKGMLPDEKRNHIVLSMIAQSVYAVAGLISYPRDYTRRRRRMM 239

QY 241 QSGRKCTDINTYGTDLDCWKRIARDEGGKAFKFGAMSNVLRMGAGFVLYLDEIKKY 297

Db 240 QSGRKADINTYGTVDCKRIAKDEGAKAFKFGAMSNVLRMGAGFVLYLDEIKKY 296

RESULT 9
US-09-185-904A-31
; Sequence 31, Application US/09185904A
Referred to: WO/00060771B1

```

; GENERAL INFORMATION:
;
; APPLICANT: Anderson, Christen M.
;
; APPLICANT: Davis, Robert E.
;
; APPLICANT: Cleveland William

```

: APPLICANT: Wiley, Sandra Eileen
 : APPLICANT: Wilier, Scott W.
 : APPLICANT: Szabo, Tomas R.
 : APPLICANT: Ghosh, Soumitra S

```

:
:
: TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
:
: TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
:
: TITLE OF INVENTION: THEREFOR
:
: FILE REFERENCE: 660088.420
:

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:
:
: CURRENT APPLICATION NUMBER: 05/05/1057,504A
:
: CURRENT FILING DATE: 1998-11-03
:
: NUMBER OF SEQ ID NOS: 33
:
: SOFTWARE: FastSeq for Windows Version 3.0

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; ORG: 2D NO 21
;
; LENGTH: 297
;
; TYPE: PRP
;
; ORGANISM: Homo sapien
;

```

Query Match	89.98;	Score 1391.5;	DB 10;	Length 297;
Best Local Similarity	88.68;	Pred. No. 2.9e-142;		

QY 1 MTDALSPAKDFLAGVAAAISKTAVPAPIERYKLLLOVOHASKOTDQOYKIIDCVVR 60
| | | | | : | | | | | : | | | | |
| | | | | : | | | | | : | | | | |

QY 61 IPKEQEVLSFWRGNIANVIRKPTQALNEAFKDKYKQIFLGVDKRPQFWRRFAGNLSG 120

121 GAAGATSLCFVYPLDFARTRLADYVGKAGAREFRGLDCLVKIKYSDGSIKGIYGFNVS 180

181 VOGIITRAYFGIYDTAKMLPDPKNTHIYISWMLAQVTAVAGLSYFPDVRRRMM 240

Qy 241 QSGKGTDMYTGTLDCKWRIARDEGGKAFKPGAMS NVLRGMCAGFYLVLYDEIKKY 297

bb 240 QSGRKGADIMYTGWVDCWBRITAKNDGAKAFKPGAMS NVLRGMCAGFYLVLYDEIKKY 296

RESULT 10
US-09--801-368-252

sequence 252, application US/03601366
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert

```

: APPLICANT: Call, Brian
: APPLICANT: Hecht, Peter
: APPLICANT: Holtzman, Doug
: APPLICANT: Madden, Kevin

```

THE UNIVERSITY OF CHICAGO


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0y      126  TSLCFYVPIDFATRIAAV---GKAAGERERGLDCLVIYSDGKGLGYCFNNVQ  182
      127  :|||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      203  SSLFIYSLIDYATRIANDAKSSKKGEGGREGVLDVYKTKTLADIGALYGFATSCA  262
      204  :|||::||::||::||::||::||::||::||::||::||::||::||::||:
0y      183  GIITYRAAYFGIYDFAK-MLPDPKNTHTVISMIAQIVTAVAGLTSPEDTYRRBMQ  241
      184  :|||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      263  GIIVYTGVLFGIYDSLKPYVLGNLTGNAFLASFLLGWGITTGAGIASLPIDYARRMMT  322
      264  :|||::||::||::||::||::||::||::||::||::||::||::||::||:
      242  SGRKGTIDIMTGTGLDCMRKIRADGEGKAFKAMSNVYRGMGAFVLYLVEIK  295
      243  :|||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      323  SGGA---VYINSMDAFKQILAKKEGAKSLFKGAGANILIRAVAGAGVLSGDIQ  373
      324  :|||::||::||::||::||::||::||::||::||::||::||::||::||:

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RESULT 13
 US-10-128-714-3338
 : Sequence 3338, Application US/10128714
 : Publication NO. US20030119013A1
 : GENERAL INFORMATION:
 : APPLICANT: Jiang, Bo
 : APPLICANT: Hu, Wenqi
 : APPLICANT: Tishkoff, Daniel
 : APPLICANT: Zamudio, Carlos
 : APPLICANT: Eroshkin, Alexey M
 : APPLICANT: Lemieux, Sebastien M
 : TITLE OF INVENTION: Identification of Essential Genes in *Aspergillus fumigatus* and
 : FILE OF INVENTION: Methods of Use
 : FILE REFERENCE: 10182-018-999
 : CURRENT APPLICATION NUMBER: US/10/128,714
 : PRIOR FILING DATE: 2002-04-23
 : PRIOR APPLICATION NUMBER: US 60/285,697
 : PRIOR FILING DATE: 2001-04-23
 : PRIOR APPLICATION NUMBER: US 60/287,066
 : PRIOR FILING DATE: 2001-04-27
 : PRIOR APPLICATION NUMBER: US 60/295,890
 : PRIOR FILING DATE: 2001-06-05
 : PRIOR APPLICATION NUMBER: US 60/303,899
 : PRIOR FILING DATE: 2001-07-09
 : PRIOR APPLICATION NUMBER: US 60/316,362
 : PRIOR FILING DATE: 2001-08-31
 : NUMBER OF SEQ ID NOS: 8603
 : SOFTWARE: PatentIn version 3.1
 : SEQ ID NO 3338
 : LENGTH: 308
 : TYPE: PRT
 : ORGANISM: *Aspergillus fumigatus*
 : US-10-128-714-3338

Query Match	47.4%;	Score 734;	DB 15;	Length 308;
Best Local Similarity	53.2%;	Pred. No. 4.7e-71;		
Matches 157;	Conservative 41;	Mismatches 85;	Indels 12;	Gaps 6;
QY	7	SEAFDFLAGVAAIAISKTAAPVIERVKLLQVHASKOITA---DKYKGIIDCVYRIIPK	63	
Db	7	AFTDSFAVGVSAAVSKTAAPIERIKLL--VQODEMIRAGRDLRDKTKGIIDCRRPAQ	64	
QY	64	EOEVLSEWGRGNNAVIRYFPQALNFAFKDKYKIOFLGVGRKQTFMRYFAGNLAGGAA	123	
Db	65	AEGVMSLRGRGTAVIRYFPQALNFAFRDYYKSMFAFKKD-RDCYAKAMMGNLASGGA	123	
QY	124	GATSLCEVYPLDFAFTRLADV--GKAGEREFRGLDCLVIKYSDDIKGHYOGFNVSV	181	
Db	124	GATSLFEPYSLDYAFTRLANDAKSAKSGGEGHFNGLIDVYRKTLASDIAGLIRREFGSV	183	
QY	182	QGIIITPAANFGIYDIKAG-MLPPPKNTHIVISMNIAQTVAVAGLSYPPDYVRRMM	240	
Db	184	LGIIVYRGLEFGMDSIKPVVLVGLSGLSFASFLLGTWTTGAGIASYPLDITIRRRMM	243	
QY	241	QSGKKGDIWTTGLDCMRKTAARDGGGAAPFKGMSNVLRMGAFVLYLDEIK	295	
Db	244	TSGEA---VYKSSLDARQIIAREGVKSLFKGAGANILRNVAGVGIYDIQV	295	

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      RESULT 14
US-10-128-714-8338
; Sequence 8338, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,637
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8338
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-8338

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Query Match      47.4%:  Score 734;  DB 15;  Length 308;
Best Local Similarity 53.2%:  Pred. No. 4.7e-71;
Match 157;  Conservative 41;  Mismatches 85;  Indels 12;  Gaps 6

QY      7 SFANDFLAGVAAAIKSTKAVAPIERVKLLQVOHASKOITA--DKOYKGIIDCVYRIIP 63
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      7 AFTDSFANGVSAANVKTAAPIERIKTL--VQNDDEMIKAGRIDRKINGIIDCRRFNAQ 64
QY      64 EQEVLSEFRGILANVIRFPTQALNFAFKDKYIKQIFLGGVDKRTQFMWYFACNLASGAA 123
      | : | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      65 AEGWMSLWRGNTANYIRFPTQALNFAFRDYYKSMFAKKD--RDGYAKMMMGNLASGAA 123
QY      124 GATSCICFPYDPDEAFATRLAADV--GKAQAREFRSLGCLVKIKYSDSIIKGLYGFENVSV 181
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      124 GATSLFEVYSIDYARTIRLANDAKSKAGGGEROFNLIDYRKRTLASDSIAGLYRFGPSV 183
QY      182 QGIIIRAAVEFGIYDTAKG-MLPDPKNHVIYSWMAQTVTAVAGLTSYFPEDYVRRRAM 240
      | : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      184 LGIYVRRLYRGMDSIKRPVVLVGSLEBSFLASFLGLTGVTVTGAGIASYPIDITIRRRMM 243
QY      241 QSGRKGDIMYTGTLDCWRKTLARDEGCAAFKGCAMSNVLRMGGAFLVLYLVEIK 295
      | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      244 TSGEA--VKYKSSIDARQIIAREGVSKLEFKGAGANILRGVAGVSLYDQVQ 295

RESULT 15
US-10-259-165-192
; Sequence 192; Application US/10259165
; Publication No. US20030135888a1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Wang, Xun
; APPLICANT: Chang, Hur-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyuki
; APPLICANT: kreps, Joel

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; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
; FILE REFERENCE: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: Patentlist.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 192
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-259-165-192

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Query Match 43.8%; Score 677.5; DB 12; Length 677;

Best Local Similarity 50.5%; Pred. No. 1.9e-64;

Matches 154; Conservative 39; Mismatches 89; Indels 23; Gaps 8;

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OY      8 FAKDFLAGVAATAISKTAVAPIERVKLLQVO-HASKQITADKQYKGLIDCVIRIPKEQE 66
DB      376 FMIDPMGVSAAVSKTAAPIERIKLQNDDEIKSGRLSHPKGIADCFGRITKDEG 435
OY      67 VLSFWRGLANVIRYEPQALNFAFKDYKQIFLAGVDKRTQFWRYPFAGNLASGCAGAT 126
DB      436 VIALMRGNTANVIRYEPQALNFAFKDHFNFNFKKDK-DGYWKMFAGNLASGCAAGAC 494
OY      127 SLCFYPLDFARTRLAD--VGKAGAREFRGLGDCLVKIKSDGKIGLYGF-NVSYQG 183
DB      495 SLFEVYSLDYARTRLANDAKAKKGGKQFNGLDVYRKTLASDSIAGLYPWIQHLPLV 554
OY      184 IITRAAYFGIYDPAK----GMLPDPKNTHIVISMTAQVTAVAGLTSYPEDTVRRRM 238
DB      555 SLNNGLYFGMYDSLKPVLVGNLQD---NFLASFLGWTITGGLASTYPIDTVRRRM 610
OY      239 MMQSGRKGTDMYTGTLDCMKRIARDEGKAFPKGAMSNVLRGMGAFVLVLYDEI---- 294
DB      611 MMTSGEA---VKYNSSIDAFKQIVAKEGAKSLFKGAGANILRAVAGAGVLGYDKLQVVV 667
OY      295 --KKY 297
DB      668 FGKKY 672

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Search completed: August 28, 2003, 19:45:24

Job time : 20.355 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 19:35:01 ; Search time 20.6898 Seconds

(without alignments)
1385.139 Million cell updates/sec

Title: US-09-811-132-32

Perfect score: 1347

Sequence: 1 MTDALSFADKDFLAGVAAA.....LRGMGAFVLYDEIKKKT 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1547	100.0	298	1 A29132	ADP, ATP carrier pr
2	1479	95.6	298	2 S31814	ADP, ATP carrier pr
3	1458	94.2	298	2 B43646	ADP, ATP carrier pr
4	1454	94.0	298	1 S03894	ADP, ATP carrier pr
5	1419	91.7	298	1 XWBO	ADP, ATP carrier pr
6	1417	91.6	298	2 S37210	ADP, ATP carrier pr
7	1417	91.6	298	2 S37210	ADP, ATP carrier pr
8	1413	91.3	298	1 A44778	adenine nucleotide
9	1170	75.6	301	1 S31935	ADP, ATP carrier pr
10	1032	66.7	300	2 T25371	hypothetical prote
11	1029	66.5	313	2 T23207	hypothetical prote
12	1029	66.5	313	2 T23207	hypothetical prote
13	986	63.7	300	2 T15206	hypothetical prote
14	968	62.6	339	2 A41677	ADP, ATP carrier pr
15	938	60.6	301	2 S51132	ADP, ATP carrier pr
16	771	49.8	386	2 T09709	ADP, ATP carrier pr
17	770	49.8	386	2 T40526	ADP, ATP carrier pr
18	765	49.5	308	1 S30259	ADP, ATP carrier pr
19	761.5	49.2	307	2 A36582	ADP, ATP carrier pr
20	759	49.1	326	2 T25728	hypothetical prote
21	759	49.1	387	2 S14876	ADP, ATP carrier pr
22	757	48.9	313	1 XWNG	ADP, ATP carrier pr
23	754	48.7	386	2 S17917	ADP, ATP carrier pr
24	753	48.7	387	2 S16568	ADP, ATP carrier pr
25	752.5	48.6	318	1 A31978	ADP, ATP carrier pr
26	752	48.6	386	2 S21974	ADP, ATP carrier pr
27	749.5	48.4	305	2 S68154	ADP, ATP carrier pr
28	749.5	48.4	306	2 T20012	hypothetical prote
29	746	48.2	306	2 T42011	ADP, ATP carrier pr

30	746	48.2	379	2 T04608	ADP, ATP carrier pr
31	745.5	48.2	385	1 S29852	ADP, ATP carrier pr
32	745	48.2	382	2 S33630	ADP, ATP carrier pr
33	741.5	47.9	379	2 S21313	ADP, ATP carrier pr
34	741.5	47.9	386	2 S14874	ADP, ATP carrier pr
35	728	47.1	309	2 A24849	ADP, ATP carrier pr
36	665.5	43.0	298	2 T24029	ADP, ATP carrier pr
37	521.5	32.7	327	2 T51577	ADP, ATP carrier pr
38	388	25.1	325	2 T04273	hypothetical prote
39	372	24.0	381	2 T51158	hypothetical prote
40	372	24.0	415	2 T48171	hypothetical prote
41	356	23.0	352	2 T01729	hypothetical prote
42	350	22.6	475	2 T50686	mitochondrial solu
43	340	22.0	358	2 T45934	peroxisomal Ca-dep
44	334	21.6	348	2 D84798	hypothetical prote
45	322.5	20.8	332	2 T47703	probable mitochond
					Ca-dependent solut

ALIGNMENTS

RESULT 1

A29132

ADP, ATP carrier protein T2 - human

N:Alternate names: mitochondrial ADP, ATP translocase 2

C:Species: Homo sapiens (man)

C>Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000

C:Accession: A29132; C28116

R:Battni, R.; Ferrarri, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.

J. Biol. Chem. 262, 4355-4359, 1987

A:Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regu

A:Reference number: A29132; MIDID:87166056; PMID:3031073

A:Accession: A29132

A:Molecule type: mRNA

A:Residues: 1-298 <BAT>

A:Cross-references: GB:U02683; NID:9179246; PIDN:AAA3579.1; PID:9179247

R:Houdsworth, J.; Altardi, G.

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1

A:Reference number: A94197; MIDID:88124845; PMID:2829183

A:Accession: C28116

A:Molecule type: mRNA

A:Residues: 47-65, 'G', '67-110, 'L', '112-161, 'G', '163-298 <HOU>

A:Cross-references: GB:U03591; NID:9339720; PIDN:AAA36749.1; PID:9339721

A:Experimental source: clone PHAT3

C:Genetics:

A:Gene: GDB:ANT2; T3; 2F1

A:Cross-references: GDB:125190; OMIM:300150

A:Map position: Xq13-Xq26

A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G

C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein

F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACPr>

F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACPr>

F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACPr>

Query Match 100.0%; Score 1547; DB 1; Length 298;

Best local Similarity 100.0%; Pred. No. 4e-130;

Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTDALISFAKDFLAGVAAAISKTAVAPIERVKLLQVHASKQITADROYKGIIDCVVR	60
DB	1	MTDALISFAKDFLAGVAAAISKTAVAPIERVKLLQVHASKQITADROYKGIIDCVVR	60
QY	61	IREDEEVLSFWNGNLNANVIRYPTQALNFAFDKVIQIFLGVDKRTQWRFPAGMLASG	120
DB	61	IREDEEVLSFWNGNLNANVIRYPTQALNFAFDKVIQIFLGVDKRTQWRFPAGMLASG	120
QY	121	GAAGATSLCFVYPLDPAFRLADVGKAGAREFRIGCLVITYSDIKGIYGFENVS	180
DB	121	GAAGATSLCFVYPLDPAFRLADVGKAGAREFRIGCLVITYSDIKGIYGFENVS	180
QY	181	VOGIIYRAAYFGIYDTAKGMLPDPKNTIHIVSMIAQTAVAGLTSYFPDTRRRMM	240

Db 61 IPKRGVLSFWRGNLANVIRFPFOALNFAFKDKYKQFLGCVNDKHQFMFRFAGNLASG 120
 Qy 121 GAAGATSLCFEYYPPLDFARTRLADVGKAGAREFERGLDCLVKIYKSDGKGLYOGFNV 180
 Db 121 GAAGATSLCFEYYPPLDFARTRLADVGKAGAREFERGLDCLVKIYKSDGKGLYOGFNV 180
 Qy 181 VGGIITIRAAVFGIYDPAKGMPLPDPKNTNHYISWMIAGTVAVAGLSTPDPDYARRMM 240
 Db 181 VGGIITIRAAVFGIYDPAKGMPLPDPKNTNHYISWMIAGTVAVAGLSTPDPDYARRMM 240
 Qy 241 OSGRKGTIDIMYTGFLDCWRKTLARDEGKAFKFGAMSNVLRMGCAFVLYLDELTKK 296
 Db 241 OSGRKGTIDIMYTGFLDCWRKTLARDEGKAFKFGAMSNVLRMGCAFVLYLDELTKK 296

RESULT 5

XMO

ADP, ATP carrier protein T1 - bovine
 N:Alternate names: ADP/ATP translocase T1
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 14-Nov-1993 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999
 C:Accession: A43646; A24822; A03181; A61343; S69369
 R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989
 A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MUID:89229093; PMID:2540808
 A:Accession: A43646
 A:Molecule type: mRNA
 A:Residues: 1-298 <POW>
 A:Cross-references: GB:M4102; NID:g529414; PIDN:AAA30768.1; PID:g529415
 R:Rasmussen, U.B.; Wohlrad, H.
 Biochem. Biophys. Res. Commun. 138, 850-857, 1986
 A:Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual
 A:Reference number: A24822; MUID:86295775; PMID:3017341
 A:Accession: A24822
 A:Molecule type: mRNA
 A:Residues: 208-298 <RAS>
 A:Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1; PID:g162631
 R:Aquila, H.; Mistr, D.; Eulitz, M.; Klingenberg, M.
 Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
 A:Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondrion
 A:Reference number: A03181; MUID:82188267; PMID:7076130
 A:Accession: A03181
 A:Molecule type: protein
 A:Residues: 2-51, 'X', '53-70', 'X', '72-109', 'X', '111-298 <ADU>
 A:Note: residue 52 may be methyllysine
 R:Babel, W.; Wachter, E.; Aquila, H.; Klingenberg, M.
 Biochim. Biophys. Acta 670, 176-180, 1981
 A:Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitochondrion
 A:Reference number: A61343; MUID:82046808; PMID:6271240
 A:Accession: A61343
 A:Molecule type: protein
 A:Residues: 205-298 <BAB>
 R:Oettmeier, W.; Masson, K.; Kalina, S.
 Eur. J. Biochem. 227, 730-733, 1995
 A:Title: [(3)H]-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP
 A:Reference number: S69369; MUID:95172058; PMID:7867632
 A:Accession: S69369
 A:Molecule type: protein
 A:Residues: 49-63,154-168 <OET>
 C:Comment: This protein is synthesized in the cytosol and transported into the mitochondrion
 C:Complex: homodimer
 C:Function:
 A:Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera
 A:Note: located in the inner mitochondrial membrane
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitoch
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
 F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
 F:52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 91.7%; Score 1419; DB 1; Length 298;
 Best Local Similarity 89.6%; Pred. No. 1e-118;
 Matches 267; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MTDALSPAKDPLAGVAAATSKTAVARIEVKLLQVHASKQITADKOKGIIIDCYVR 60
 Db 1 MSDQALSPKDFLAGVAAATSKTAVARIEVKLLQVHASKQISAKOKGIIIDCYVR 60
 Qy 61 IPKEGVLSFWRGNLANVIRFPFOALNFAFKDKYKQFLGCVNDKHQFMFRFAGNLASG 120
 Db 61 IPKEGVLSFWRGNLANVIRFPFOALNFAFKDKYKQFLGCVNDKHQFMFRFAGNLASG 120
 Qy 121 GAAGATSLCFEYYPPLDFARTRLADVGKAGAREFERGLDCLVKIYKSDGKGLYOGFNV 180
 Db 121 GAAGATSLCFEYYPPLDFARTRLADVGKAGAREFERGLDCLVKIYKSDGKGLYOGFNV 180
 Qy 181 VGGIITIRAAVFGIYDPAKGMPLPDPKNTNHYISWMIAGTVAVAGLSTPDPDYARRMM 240
 Db 181 VGGIITIRAAVFGIYDPAKGMPLPDPKNTNHYISWMIAGTVAVAGLSTPDPDYARRMM 240
 Qy 241 OSGRKGTIDIMYTGFLDCWRKTLARDEGKAFKFGAMSNVLRMGCAFVLYLDELTKK 297
 Db 241 OSGRKGTIDIMYTGFLDCWRKTLARDEGKAFKFGAMSNVLRMGCAFVLYLDELTKK 297

RESULT 6

S37210

ADP, ATP carrier protein T1 - mouse
 N:Alternate names: adenine nucleotide carrier
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
 C:Accession: S37210
 R:Riaplance, C.; Costet, P.
 submitted to the EMBL Data Library, September 1993
 A:Reference number: S37210
 A:Accession: S37210
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <RAP>
 A:Cross-references: EMBL:X74510; NID:g402627; PIDN:CAA52616.1; PID:g402628
 C:Genetics:
 A:Gene: ANCI
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 91.6%; Score 1417; DB 2; Length 298;
 Best Local Similarity 89.6%; Pred. No. 1.5e-118;
 Matches 266; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MTDALSPAKDPLAGVAAATSKTAVARIEVKLLQVHASKQITADKOKGIIIDCYVR 60
 Db 1 MGDQALSPKDFLAGVAAATSKTAVARIEVKLLQVHASKQISAKOKGIIIDCYVR 60
 Qy 61 IPKEGVLSFWRGNLANVIRFPFOALNFAFKDKYKQFLGCVNDKHQFMFRFAGNLASG 120
 Db 61 IPKEGVLSFWRGNLANVIRFPFOALNFAFKDKYKQFLGCVNDKHQFMFRFAGNLASG 120
 Qy 121 GAAGATSLCFEYYPPLDFARTRLADVGKAGAREFERGLDCLVKIYKSDGKGLYOGFNV 180
 Db 121 GAAGATSLCFEYYPPLDFARTRLADVGKAGAREFERGLDCLVKIYKSDGKGLYOGFNV 180
 Qy 181 VGGIITIRAAVFGIYDPAKGMPLPDPKNTNHYISWMIAGTVAVAGLSTPDPDYARRMM 240
 Db 181 VGGIITIRAAVFGIYDPAKGMPLPDPKNTNHYISWMIAGTVAVAGLSTPDPDYARRMM 240
 Qy 241 OSGRKGTIDIMYTGFLDCWRKTLARDEGKAFKFGAMSNVLRMGCAFVLYLDELTKK 297
 Db 241 OSGRKGTIDIMYTGFLDCWRKTLARDEGKAFKFGAMSNVLRMGCAFVLYLDELTKK 297

QY 8 FAKDFLAGVAAAIKSTAVAPIERVKLLQVQASHAKQITADKQYKGIIDCVARIPKEQEV 67
 Db 25 FLIDLASGGTAAGVAAVSTAAVAPIERVKLLQVQASHAKQITADKQYKGIIDCVARIPKEQEV 84
 QY 68 LSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASGAAGATS 127
 Db 85 AALMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASGAAGATS 144
 QY 128 LCFVYPLDPAFRTLRADAVGKAGAEERFGLGDLVIRYSDGKIGLYOGFNVSVQGIIT 187
 Db 145 LCFVYPLDPAFRTLRADAVGKAN-EREFKGLADCLVIAKSDGPIGLYRGFVSVQGIIT 203
 QY 188 RAAYFGIYDTAKGML-PDPRKNTIIVISWMAIQVTAVAGLITSPFPTVRRMMQSGRGK 246
 Db 204 RAAYFGMFTAKKVFADGKRLNFAFAMAIAQVYVYSGSLTSPMDTVRRMMQSGRGK- 262
 QY 247 TDIMYGTLLDCWKRIRADEGKAFKAGMSNVLRGAGAFVLYLVEIKKY 297
 Db 263 -DLYKNTLDCVAKIKINEGMSAMFKGALSNVRGIGALVLYLVEIKKF 312

RESULT 13
 T15206
 hypothetical protein W02D3.6 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
 C:Accession: T15206
 R:Le, T.; Weinstock, L.; Rikkin, L.
 submitted to the EMBL Data Library, May 1997
 A:Description: The sequence of C. elegans cosmid W02D3.
 A:Reference number: Z18308
 A:Accession: T15206
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-300 <LEFT>
 A:Cross-references: EMBL:AF003141; NID:92088732; PID:92088738; PIDN:AAB54179.1; GSPDB:GN
 A:Experimental source: strain Bristol NZ; clone W02D3
 C:Genetics:
 A:Gene: CESP:W02D3.6
 A:Map position: 1
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 F:9-103/Domain: ADP/ATP carrier protein repeat homology <ACR>

Query Match 63.7%; Score 986; DB 2; Length 300;
 Best Local Similarity 67.5%; Pred. No. 3, 6e-60;
 Matches 195; Conservative 32; Mismatches 58; Indels 4; Gaps 3;
 QY 8 FAKDFLAGVAAAIKSTAVAPIERVKLLQVQASHAKQITADKQYKGIIDCVARIPKEQEV 67
 Db 12 FLIDLASGGTAAGVAAVSTAAVAPIERVKLLQVQASHAKQITADKQYKGIIDCVARIPKEQEV 71
 QY 68 LSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASGAAGATS 127
 Db 72 AAFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASGAAGATS 131
 QY 128 LCFVYPLDPAFRTLRADAVGKAGAEERFGLGDLVIRYSDGKIGLYOGFNVSVQGIIT 187
 Db 132 LCFVYPLDPAFRTLRADAVGK-GEVREFQGLTDFCVIRYSDGPIGLYRGFVSVQGIIT 190
 QY 188 RAAYFGIYDTAKGML-PDPRKNTIIVISWMAIQVTAVAGLITSPFPTVRRMMQSGRGK 246
 Db 191 RAAYFGMFTAKKVFADGKRLNFAFAMAIAQVYVYSGSLTSPMDTVRRMMQSGRGK- 249
 QY 247 TDIMYGTLLDCWKRIRADEGKAFKAGMSNVLRGAGAFVLYLVEIKKY 295
 Db 250 -DLYKNTLDCVAKIKINEGMSAMFKGALSNVRGIGALVLYLVEIKQ 297

RESULT 14
 A41677
 ADP/ATP carrier protein - *Chlorella kessleri*
 C:Species: *Chlorella kessleri*
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999

C:Accession: A41677
 R:Higharth, C.; Sauer, N.; Tanner, W.
 J. Biol. Chem. 266, 24044-24047, 1991
 A:Title: Glucose increases the expression of the ATP/ADP translocator and the glycera
 A:Reference number: A41677, PMID:92084708; PMID:1748677
 A:Accession: A41677
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-339 <HIT>
 A:Cross-references: GB:M76669; NID:9516596; PIDN:AAA33027.1; PID:9516597
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:38-134/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F:144-235/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:241-329/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 62.6%; Score 968; DB 2; Length 339;
 Best Local Similarity 65.8%; Pred. No. 1, 7e-78;
 Matches 194; Conservative 29; Mismatches 64; Indels 8; Gaps 5;
 QY 6 LSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASGAAG 63
 Db 39 MAFVKDLAGGTAGTAAIKSTAVAPIERVKLLQVQASHAKQITADKQYKGIIDCVARIPK 98
 QY 64 EDEVLSEFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASGAAG 123
 Db 99 EGVASLFWGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASGAAG 157
 QY 124 GATSLCFVYPLDPAFRTLRADAVGKAGAEERFGLGDLVIRYSDGKIGLYOGFNVSVQ 183
 Db 158 GAGSLIYVPLDPAFRTLRADAVG-SEKSEFEGVLVCLSKYVKKRGPMLYQGFVSVQ 216
 QY 184 IIVRAAYFGIYDTAKGML-PDPRKNTIIVISWMAIQVTAVAGLITSPFPTVRRMMQSG 242
 Db 217 IIVRAAYFGIYDTAKGML-PDPRKNTIIVISWMAIQVTAVAGLITSPFPTVRRMMQSG 276
 QY 243 GRGRTIIMTGTITDCWKRIRADEGKAFKAGMSNVLRGAGAFVLYLVEIKKY 297
 Db 277 --GGEROYNLTIDCWKRIRADEGKAFKAGMSNVLRGAGAFVLYLVEIKKF 328

RESULT 15
 S51132
 ADP/ATP carrier protein - malaria parasite (Plasmodium falciparum)
 N:Alternate names: ADP/ATP transporter
 C:Species: *Plasmodium falciparum*
 C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jun-2000
 C:Accession: S68993; S51132
 R:Hall, T.; Jaureguiberry, G.
 Eur. J. Biochem. 228, 86-91, 1995
 A:Title: Molecular characterisation of the ADP/ATP-transporter cDNA from the human ma
 A:Reference number: S68993; PMID:95188918; PMID:7883016
 A:Accession: S68993
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-301 <HIT>
 A:Cross-references: EMBL:X83551; NID:9623334; PIDN:CAA58541.1; PID:9623335
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 F:6-102/Domain: ADP/ATP carrier protein repeat homology
 F:112-203/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F:209-301/Domain: ADP/ATP carrier protein repeat homology <ACP2>

Query Match 60.6%; Score 938; DB 2; Length 301;
 Best Local Similarity 61.2%; Pred. No. 6, 8e-76;
 Matches 183; Conservative 43; Mismatches 67; Indels 6; Gaps 5;
 QY 2 TDAALSFANDFLAGVAAAIKSTAVAPIERVKLLQVQASHAKQITADKQYKGIIDCVARIP 59
 Db 3 SDIKTNFAADFLMGISAAIKSTAVAPIERVKLLQVQASHAKQITADKQYKGIIDCVARIP 62
 QY 60 RPKDEVLSEFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLAS 119

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Db      63 RVSKEQVLSLRGNVAVYIRFPYQAFNFAEKDYFKNIF-PRYDQNTDESKFEVCVNILS 121
QY      120 GGAAGATSLCFVYPLDFAFTRLADVGKAGAREFERGLDCLVKIYKSDGINKLYOGFNV 179
      122 GATAGATSLILYVPLDFAFTRLASDIGNK-GKDRQFTGLEFDCLAKIYKQGTGLSLISGFCV 180
Db      180 SVQGIITIRAAVEFGIYDTAKGML-PDPKNTHTIVISMMIAQVTAVAGLTSYPPDVTVRRRM 238
      181 SVTGIIYVYRGSYFGLYDSAKALLFTNDKNTNIVLKWAVASVYIILAGLISYPPDVTVRRRM 240
QY      239 MMQSGRKG-TDIMYGTGLDCWRKTIARDEGKAFKFGAMSNNLRGAGAFVLYLYDEIKK 296
Db      241 MMMSGRKKEETQYKNTIDCWIKILRNESGFKGFEKGAWANVIRGAGGALVLYFYDELOK 299

```

Search completed: August 28, 2003, 19:43:17
 Job time : 20.6898 secs

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OM protein - protein search, using sw model

Run on: August 28, 2003, 19:28:06 ; Search time 12.0134 Seconds

(without alignments)
1166.524 Million cell updates/sec

Title: US-09-811-132-32

Perfect score: 1547

Sequence: 1 MTDALSFADFLAGVAAA.....LRGMGAFVLVDEIKRYT 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1537	99.4	298	ADP2_HUMAN	P05141 homo sapien
2	1525	98.6	298	ADP2_RAT	Q09073 rattus norv
3	1519	98.2	298	ADP2_MOUSE	P51881 mus musculu
4	1458	94.2	298	ADP3_BOVIN	P32007 bos taurus
5	1454	94.0	298	ADP3_HUMAN	P12336 homo sapien
6	1417	91.6	298	ADP1_MOUSE	P48962 mus musculu
7	1417	91.6	298	ADP1_RAT	Q05662 rattus norv
8	1414	91.4	297	ADP1_BOVIN	P02722 bos taurus
9	1413	91.3	298	ADP1_HUMAN	P12235 homo sapien
10	1253.5	81.0	299	ADP_DROME	Q26365 drosophila
11	1190	76.9	301	ADP_ANOGA	Q27365 anopheles g
12	968	62.6	339	ADP_CHLKE	P31692 chlorella k
13	771	49.8	386	ADP1_GOSHI	Q22342 gossypium h
14	770	49.8	322	ADP_SCHPO	Q09188 schizosacch
15	765	49.5	308	ADP_CHLRE	P27080 chlamydomon
16	761.5	49.2	307	ADP3_YEAST	P18238 saccharomyc
17	759	48.9	387	ADP1_MAIZE	P04709 zea mays (m
18	757	48.9	313	ADP1_NECUR	P02723 neosporea
19	753.5	48.7	385	ADP2_ARATH	P40941 arabidopsis
20	753	48.7	387	ADP2_MAIZE	P12857 zea mays (m
21	752.5	48.6	318	ADP2_YEAST	P25083 solanum tub
22	752	48.6	386	ADP1_SOLUT	P31691 oryza sativ
23	750	48.5	382	ADP_ORYSA	P41301 solanum tub
24	749.5	48.4	305	ADP1_KLUTA	P49382 kluyveromyc
25	747.5	48.3	381	ADP1_ARATH	P31167 arabidopsis
26	744	48.1	331	ADP1_WHEAT	Q4129 triticum ae
27	741.5	47.9	386	ADP2_SOLUT	P27081 solanum tub
28	737	47.6	331	ADP2_WHEAT	Q4130 triticum ae
29	728	47.1	309	ADP1_YEAST	P04710 saccharomyc
30	312.5	20.2	565	CMG3_CAEEL	P19529 caenorhabd
31	307	19.8	588	CMG2_CAEEL	Q20799 caenorhabd
32	285	18.4	330	GDC_BOVIN	Q01888 bos taurus
33	284	18.4	307	ODC2_YEAST	Q09297 saccharomyc

34	278	18.0	325	1	UCP5_MOUSE	Q922b2 mus musculu
35	276.5	17.9	322	1	GDC_RAT	P16261 rattus norv
36	276.5	17.9	702	1	CMG1_CAEEL	Q21153 caenorhabd
37	276	17.8	678	1	CMG1_HUMAN	Q95746 homo sapien
38	274	17.7	325	1	UCP5_HUMAN	Q95258 homo sapien
39	265.5	17.2	332	1	GDC_HUMAN	P16260 homo sapien
40	265	17.1	306	1	CN69_MOUSE	Q8bi03 mus musculu
41	261.5	16.9	675	1	CMG2_HUMAN	Q94j50 homo sapien
42	261	16.9	310	1	ODC1_YEAST	Q03028 saccharomyc
43	257.5	16.6	315	1	MPL_HUMAN	Q9h2d1 homo sapien
44	256	16.5	303	1	CN69_HUMAN	Q8n8r3 homo sapien
45	249.5	16.1	326	1	YB08_SCHPO	O13805 schizosacch

ALIGNMENTS

RESULT 1
ADP2_HUMAN STANDARD; PRT; 298 AA.
ID ADP2_HUMAN
AC P05141; O43350;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP, ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90375457; PubMed=2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wurzel J.;
RT "The human fibroblast adenine nucleotide translocator gene. Molecular
cloning and sequence."
RL J. Biol. Chem. 265:16060-16063(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87166056; PubMed=3031073;
RA Batini R., Ferrati S., Kaczmarek L., Calabretta B., Chen S.T.,
RA Baserga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
growth-regulated."
RL J. Biol. Chem. 262:4355-4358(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX Chen C.N., Su Y., Baybayan P., Siruno A., Nagara J. R.,
RA Mazarella R.A., Schlessinger D., Chen E.Y.;
RT Submitted (JUN-1996) to the EMBL/GenBank/DBD databases.
RN [4]
RP SEQUENCE FROM N.A.
RX Becker M., Graves T., Ozersky P.;
RT Submitted (JAN-1998) to the EMBL/GenBank/DBD databases.
RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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CC -----
 CC EMBL; M57424; AAA51737.1; -
 CC DR EMBL; J02683; AAA35579.1; -
 CC DR EMBL; L78810; AAB39266.1; -
 CC DR EMBL; AC004000; AAB96347.1; -
 CC DR EMBL; J03591; AAA36749.1; -
 CC DR PIR; A29132; A29132.
 CC DR Genew; HGNC:10991; SLC25A5.
 CC DR MIM; 300150; -
 CC DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 CC DR GO; GO:0015207; F: adenine transporter activity; TAS.
 CC DR GO; GO:0006832; P: small molecule transport; TAS.
 CC DR InterPro; IPR002067; Mlt_carrier.
 CC DR InterPro; IPR002030; Mlt_uncoupling.
 CC DR Pfam; PF00153; mlt_carr; 3.
 CC DR PRINTS; PR00926; MITOCARRIER.
 CC DR PRINTS; PR00784; MTUNCOUPLING.
 CC DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 CC KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 CC Multigene family.
 CC FT TRANSMEM 12 29 1 (POTENTIAL).
 CC FT TRANSMEM 73 91 2 (POTENTIAL).
 CC FT TRANSMEM 117 134 3 (POTENTIAL).
 CC FT TRANSMEM 176 195 4 (POTENTIAL).
 CC FT TRANSMEM 214 231 5 (POTENTIAL).
 CC FT TRANSMEM 273 291 6 (POTENTIAL).
 CC FT REPEAT 1 111 1.
 CC FT REPEAT 112 208 2.
 CC FT REPEAT 209 298 3.
 CC FT CONFLICT 6 6 V -> L (IN REF. 2).
 CC FT CONFLICT 66 66 G -> E (IN REF. 2).
 CC FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
 CC FT CONFLICT 162 162 V -> G (IN REF. 5).
 CC FT SEQUENCE 298 AA; 32895 MM; F973C3AED92C49D3 CRC64;
 CC SQ

Query Match 99.4%; Score 1537; DB 1; Length 298;
 Best Local Similarity 99.3%; Pred. No. 8.9e-128;
 Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTDAAISFAKDFLAGVAAAIKTAIVAPIERVKLLQOVASKOITADKOYKGIIDCVR 60
 DB 1 MTDAAVSFAKDFLAGVAAAIKTAIVAPIERVKLLQOVASKOITADKOYKGIIDCVR 60
 QY 61 IPKEQVLSFWRGMLANVIRYFPQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
 DB 61 IPKEQVLSFWRGMLANVIRYFPQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADYVKAAGEFERGIGDCLVYIKSDGKIGLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADYVKAAGEFERGIGDCLVYIKSDGKIGLYOGFNVS 180
 QY 181 VOGIIIRAAVFGIYDTAKMLPDPKNTHTVISMIAQYTAVAGLSTYFPDVRRRMM 240
 DB 181 VOGIIIRAAVFGIYDTAKMLPDPKNTHTVISMIAQYTAVAGLSTYFPDVRRRMM 240
 QY 241 QSGKRGTDIMYTGILDCMRKIARDEGKAFKGAWSNVLRMGCGAFVLVYDEIKKYY 298
 DB 241 QSGKRGTDIMYTGILDCMRKIARDEGKAFKGAWSNVLRMGCGAFVLVYDEIKKYY 298

RESULT 2
 ADT2_RAT STANDARD; PRT; 298 AA.
 ID ADT2_RAT
 AC 009073;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 GN SLC25A5 OR ANT2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE-Liver;
 RX MEDLINE=94002161; Pubmed=8399300;
 RA Shinohara Y., Kamida M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 RT encoding rat mitochondrial adenine nucleotide translocator.";
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1 PUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1 SUBUNIT: Homodimer.
 CC -1 SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1 TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
 CC SKELETAL MUSCLE.
 CC -1 DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1 SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
 CC CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC -----
 CC EMBL; D12771; BAA02338.1; -
 CC DR InterPro; IPR002067; Mlt_carrier.
 CC DR InterPro; IPR002030; Mlt_uncoupling.
 CC DR InterPro; IPR001993; Mitoch_carrier.
 CC DR Pfam; PF00153; mlt_carr; 3.
 CC DR PRINTS; PR00926; MITOCARRIER.
 CC DR PRINTS; PR00784; MTUNCOUPLING.
 CC DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 CC KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 CC Multigene family.
 CC FT TRANSMEM 12 29 1 (POTENTIAL).
 CC FT TRANSMEM 73 91 2 (POTENTIAL).
 CC FT TRANSMEM 117 134 3 (POTENTIAL).
 CC FT TRANSMEM 176 195 4 (POTENTIAL).
 CC FT TRANSMEM 214 231 5 (POTENTIAL).
 CC FT TRANSMEM 273 291 6 (POTENTIAL).
 CC FT REPEAT 1 111 1.
 CC FT REPEAT 112 208 2.
 CC FT REPEAT 209 298 3.
 CC FT SEQUENCE 298 AA; 32901 MM; 6A59204B987EFE35 CRC64;
 CC SQ

Query Match 98.6%; Score 1525; DB 1; Length 298;
 Best Local Similarity 98.3%; Pred. No. 1e-126;
 Matches 293; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDAAISFAKDFLAGVAAAIKTAIVAPIERVKLLQOVASKOITADKOYKGIIDCVR 60
 DB 1 MTDAAVSFAKDFLAGVAAAIKTAIVAPIERVKLLQOVASKOITADKOYKGIIDCVR 60
 QY 61 IPKEQVLSFWRGMLANVIRYFPQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
 DB 61 IPKEQVLSFWRGMLANVIRYFPQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADYVKAAGEFERGIGDCLVYIKSDGKIGLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADYVKAAGEFERGIGDCLVYIKSDGKIGLYOGFNVS 180
 QY 181 VOGIIIRAAVFGIYDTAKMLPDPKNTHTVISMIAQYTAVAGLSTYFPDVRRRMM 240
 DB 181 VOGIIIRAAVFGIYDTAKMLPDPKNTHTVISMIAQYTAVAGLSTYFPDVRRRMM 240

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DB      191 VGGIIYRAAYFGIYDPAKGMIPDPKNTHIFISWIAOSVTAAGLTSTPDTVRRMM 240
QY      241 OSGRKGTDMYGTGLDCKRKIARDGSKAFKFGAMSNVLRGGAFLVLYDEIRKKT 298
DB      241 OSGRKGTDMYGTGLDCKRKIARDGSKAFKFGAMSNVLRGGAFLVLYDEIRKKT 298

RESULT 3
ADT2_MOUSE STANDARD: PRT: 298 AA.
AC      P51881.061311.
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DE      28-FEB-2003 (Rel. 41, Last annotation update)
DE      ADP,ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE      (Adenine nucleotide translocator 2) (ANT 2).
GN      SLG25A5 OR ANT2.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6; TISSUE=Brain;
RX      MEDLINE=97059403; PubMed=8903724;
RA      Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT      "Rapid evolution of human pseudautosomal genes and their mouse
RT      homologs."
RL      Mamm. genome 7:25-30(1996).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Skeletal muscle;
RA      Sheldon J.G.;
RL      Theiss (1995), University of Cambridge, U.K.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/SV;
RA      Costet P., Laplace C.;
RL      Submitted (FEB-1993) to the EMBL/Genbank/DBJ databases.
RN      [4]
RP      REVISIONS.
RA      Laplace C.;
RL      Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
RN      [5]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=20432087; PubMed=10974536;
RA      Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT      "Expression and sequence analysis of the mouse adenine nucleotide
RT      translocase 1 and 2 genes."
RL      Gene 254:57-66(2000).
CC      -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC      MITOCHONDRIAL INNER MEMBRANE.
CC      -1- SUBUNIT: Homodimer.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC      inner membrane.
CC      -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC      -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC      -----
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CC      or send an email to license@sdb.ch).
CC      -----
DR      EMBL: U27316; AAC52838.1; -
DR      EMBL: U10404; AAA19009.1; -
DR      EMBL: X70847; CAA50196.1; -
DR      EMBL: AF240003; AAF64471.1; -
DR      MGD: MGI:1353496; SLC25A5.
DR      InterPro: IPR002067; Mtc_carrier.
DR      InterPro: IPR002030; Mtc_uncoupling.

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DR      InterPro: IPR001993; MitoCh_carrier.
DR      Pfam: PF00153; mto_carr. 3.
DR      PRINTS: PR00926; MITOCARRIER.
DR      PRINTS: PR00784; MTUNCOUPLING.
DR      PROSITE: PS00215; MITOCH_CARRIER. 3.
KW      Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW      Multigene family.
FT      TRANSMEM 12 29 1 (POTENTIAL).
FT      TRANSMEM 73 91 2 (POTENTIAL).
FT      TRANSMEM 117 134 3 (POTENTIAL).
FT      TRANSMEM 176 195 4 (POTENTIAL).
FT      TRANSMEM 214 231 5 (POTENTIAL).
FT      TRANSMEM 273 291 6 (POTENTIAL).
FT      REPEAT 1 111 1.
FT      REPEAT 112 208 2.
FT      REPEAT 209 298 3.
SQ      SEQUENCE 298 AA; 32931 MW; 0798E04B987EE20 CRC64;

Query Match      98.2%; Score 1519; DB 1; Length 298;
Best Local Similarity 98.0%; Pred. No. 3.4e-126;
Matches 292; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 MTDAAISFAKDFLAGGVAALISKTAVAPIERVKLLQVOHASKQITADKQYGIIDCVVR 60
DB      1 MTDAAVSFAKDFLAGGVAALISKTAVAPIERVKLLQVOHASKQITADKQYGIIDCVVR 60
QY      61 IPKEGVSEFWRGANLANYRYEPTQALNFAFDKQKQIFLGVDVDRQTFWRFAGNLSG 120
DB      61 IPKEGVSEFWRGANLANYRYEPTQALNFAFDKQKQIFLGVDVDRQTFWRFAGNLSG 120
QY      121 GAAGATSLCFVYPLDFAFRLADYAGKAGEREPRGLDCLVKKIYKSDIKGLYOGFNV 180
DB      121 GAAGATSLCFVYPLDFAFRLADYAGKAGEREPRGLDCLVKKIYKSDIKGLYOGFNV 180
QY      181 VGGIIYRAAYFGIYDPAKGMIPDPKNTHIFISWIAOSVTAAGLTSTPDTVRRMM 240
DB      181 VGGIIYRAAYFGIYDPAKGMIPDPKNTHIFISWIAOSVTAAGLTSTPDTVRRMM 240
QY      241 OSGRKGTDMYGTGLDCKRKIARDGSKAFKFGAMSNVLRGGAFLVLYDEIRKKT 298
DB      241 OSGRKGTDMYGTGLDCKRKIARDGSKAFKFGAMSNVLRGGAFLVLYDEIRKKT 298

RESULT 4
ADT3_BOVIN STANDARD: PRT: 298 AA.
AC      P32007.
DT      01-JUL-1993 (Rel. 26, Created)
DT      01-JUL-1993 (Rel. 26, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      ADP,ATP carrier protein, isoform T2 (ADP/ATP translocase 3) (Adenine
DE      nucleotide translocator 3) (ANT 3).
GN      SLG25A6 OR ANT3.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=89229093; PubMed=2540808;
RA      Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT      "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT      differences in various tissues."
RL      Biochemistry 28:866-873(1989).
CC      -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC      MITOCHONDRIAL INNER MEMBRANE.
CC      -1- SUBUNIT: Homodimer.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC      inner membrane.
CC      -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC      -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC      -----

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 CC or send an email to license@isb-sib.ch).

DR EMBL; M24103; AAA30769.1; -
 DR PIR; B43646; B43646.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;

FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 2 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32877 MW; 1C34E7DF6EDE4061 CRC64;

Query Match 94.28; Score 1458; DB 1; Length 298;
 Best Local Similarity 92.98; Pred. No. 7.7e-121;
 Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTDALSFADFLAGVAAIAISKTAIVPIERVKLLLOVANSKOITADKOYKGIIDCVYR 60
 1 MTEBAISFADFLAGVAAIAISKTAIVPIERVKLLLOVANSKOITADKOYKGIIDCVYR 60
 DB 1 MTEBAISFADFLAGVAAIAISKTAIVPIERVKLLLOVANSKOITADKOYKGIIDCVYR 60
 QY 61 IPKEQEVLSFWRCNLAVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRYFAGNLASG 120
 61 IPKEQEVLSFWRCNLAVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRYFAGNLASG 120
 DB 61 IPKEQEVLSFWRCNLAVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFAKRLADYVGAAGAREEREGDGLVYIKKSDGKGLYOGFNVS 180
 121 GAAGATSLCFVYPLDFAKRLADYVGAAGAREEREGDGLVYIKKSDGKGLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDFAKRLADYVGAAGAREEREGDGLVYIKKSDGKGLYOGFNVS 180
 QY 181 VGGIIIRAYAFGIYDPAKGMLEDPKNTHTIVISWMIQVTAAYAGLSTYEPDVRRRMM 240
 181 VGGIIIRAYAFGIYDPAKGMLEDPKNTHTIVISWMIQVTAAYAGLSTYEPDVRRRMM 240
 DB 181 VGGIIIRAYAFGIYDPAKGMLEDPKNTHTIVISWMIQVTAAYAGLSTYEPDVRRRMM 240
 QY 241 QSGRKGTDMYTGTLDCWRKRIADDEGKAFKFGKMSVNLKMGCAFVLYLDEIKK 296
 241 QSGRKGTDMYTGTLDCWRKRIADDEGKAFKFGKMSVNLKMGCAFVLYLDEIKK 296
 DB 241 QSGRKGTDMYTGTLDCWRKRIADDEGKAFKFGKMSVNLKMGCAFVLYLDEIKK 296

RESULT 5

ADT3_HUMAN STANDARD; PRT; 298 AA.
 AC P12336; O96C49;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)
 DE (Adenine nucleotide translocator 3) (ANT 3).
 GN SLC25A6 OR ANT3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89236396; PubMed-2541251;
 RA Cozens A.L., Runswick M.J., Walker J.E.;

RT "DNA sequences of two expressed nuclear genes for human mitochondrial
 RT ADP/ATP translocase.";
 RL J. Mol. Biol. 206:261-280(1989).

[2]
 RP SEQUENCE FROM N.A.
 RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Buck J., Gibbs R.A.,
 RA Margolin J.F.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

[3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain, Cervix, Eye, and Lung;
 RX MEDLINE-22388257; PubMed-12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschuler R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Katschul S.F., Zeeberg B., Buettner R.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo A.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uadln T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Nadeau A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerker A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[4]
 RP SEQUENCE OF 36-298 FROM N.A.
 RC TISSUE-liver;
 RX MEDLINE-86124845; PubMed-2829183;
 RA Houldsworth J., Altardi G.;

RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 RT level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).

CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.

CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

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 CC or send an email to license@isb-sib.ch).

DR EMBL; J03592; AAA36750.1; -
 DR EMBL; AY007135; AAC01998.1; -
 DR EMBL; BC007295; AAH07295.1; -
 DR EMBL; BC007850; AAH07850.1; -
 DR EMBL; BC008737; AAH08737.1; -
 DR EMBL; BC008935; AAH08935.1; -
 DR EMBL; BC014775; AAH14775.1; -
 DR PIR; S03894; S03894.
 DR Genew; HGNC:10992; SLC25A6.

DR MTM; 300151; -
 DR MTM; 403000; -
 DR GO; GO:0005744; C:mitochondrial inner membrane translocase co. .; TAS.
 DR GO; GO:0005471; F:ATP/ADP antiporter activity; NAS.
 DR GO; GO:0006854; P:ATP/ADP exchange; TAS.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR InterPro: IPR001993; Mitoch_carrier.

DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 MultiGene Family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 100 1.
 FT REPEAT 101 208 2.
 FT REPEAT 209 298 3.
 FT REPEAT 105 108 3.
 FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).
 FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).
 SO SEQUENCE 298 AA; 32866 MW; 185349F0E49672F CRC64;
 Query Match 94.0%; Score 1454; DB 1; Length 298;
 Best Local Similarity 92.6%; Pred. No. 1.7e-120;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTDAALSPAKDFLAGVAAISKRAVAPIERVKLLQVHASKQITADKQKGIIDCYR 60
 DB 1 MTEQAISEPAKDFLAGVAAISKRAVAPIERVKLLQVHASKQITADKQKGIIDCYR 60
 QY 61 IPKDEYSEFWRGNLANVIRYEPQALNFARFKDKYKQIFLGVDKRRQTFMRENGNLASG 120
 DB 61 IPKDEYSEFWRGNLANVIRYEPQALNFARFKDKYKQIFLGVDKRRQTFMRENGNLASG 120
 QY 121 GAAGATSLCEFYPLDFARTRLADVGKASERFGLDCLVKIKYKSGIKGLYOGFNVS 180
 DB 121 GAAGATSLCEFYPLDFARTRLADVGKASERFGLDCLVKIKYKSGIKGLYOGFNVS 180
 QY 121 GAAGATSLCEFYPLDFARTRLADVGKASERFGLDCLVKIKYKSGIKGLYOGFNVS 180
 DB 121 GAAGATSLCEFYPLDFARTRLADVGKASERFGLDCLVKIKYKSGIKGLYOGFNVS 180
 QY 181 VGGITTRAAVFGIYDTRAKGMLPDKRNTIYISMKIAOTVAVAGLISYPEDTVRRMM 240
 DB 181 VGGITTRAAVFGIYDTRAKGMLPDKRNTIYISMKIAOTVAVAGLISYPEDTVRRMM 240
 QY 241 QSGRKGDTIMTGTLDCKRKIARDEGKAFKFGANSNVLRGGAFFVLYLDEIRK 296
 DB 241 QSGRKGDTIMTGTLDCKRKIARDEGKAFKFGANSNVLRGGAFFVLYLDEIRK 296
 DB 241 QSGRKGDTIMTGTLDCKRKIARDEGKAFKFGANSNVLRGGAFFVLYLDEIRK 296
 RESULT 6
 ADT1_MOUSE STANDARD: PRT: 298 AA.
 AC P48962; 062164;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (MANC1).
 GN SLC25A4 OR ANT1 OR ANCL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6; TISSUE-Brain;
 RX MEDLINE-97059403; PubMed-8903724;
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudautosomal genes and their mouse homologs";
 RL Mamm. Genome 7:25-30(1996).
 RP [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c; TISSUE-Muscle;
 RA Laplace C., Costet P.;
 RL Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.
 RP [3]
 RP SEQUENCE FROM N.A.

RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes";
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Eye;
 RX MEDLINE-22388257; PubMed-12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C., Brownstein M.J., Ueda T.B., Toshiyuki S., Carroll P., Scheetz T.E., Rabe S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.O., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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 CC -----
 DR EMBL; U27315; AAC52837.1; -;
 DR EMBL; X74510; CA52616.1; -;
 DR EMBL; AF240002; AAF64470.1; -;
 DR EMBL; BC003791; AAH03791.1; -;
 DR EMBL; BC026925; AAH26925.1; -;
 DR PIR; S37210; S37210.
 DR MGI; MGI:1353495; SLC25A4.
 DR InterPro; IPR002067; Mlt_carrier.
 DR InterPro; IPR002030; Mlt_uncoupling.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 MultiGene Family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 101 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 136 136 F -> L (IN REF. 1).
 FT CONFLICT 136 136 F -> L (IN REF. 1).
 SO SEQUENCE 298 AA; 32904 MW; 3A849FEAB0981462 CRC64;
 Query Match 91.6%; Score 1417; DB 1; Length 298;

Best Local Similarity 89.6%; Pred. No. 3.1e-117;
Matches 266; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTDALSFADFLAGVAAIASTKAVAPIERVKLLQVHASKQITADKQYKGIIDCVR 60
1 MGDQALSFLEDFLAGIAAIVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVR 60
Db 1 MGDQALSFLEDFLAGIAAIVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVR 60

QY 61 IPKEQVLSFWRGNLANVIRFPTQALNFAFKKQYKQIFGVDKRTQFWRPAGNLSG 120
61 IPKEQVLSFWRGNLANVIRFPTQALNFAFKKQYKQIFGVDKRTQFWRPAGNLSG 120
Db 61 IPKEQVLSFWRGNLANVIRFPTQALNFAFKKQYKQIFGVDKRTQFWRPAGNLSG 120

QY 121 GAAGATSLCFVYPLDFARTLADVCKAGAREFRGIGDCLVYIKSDGKIGLYOGFNVS 180
121 GAAGATSLCFVYPLDFARTLADVCKAGAREFRGIGDCLVYIKSDGKIGLYOGFNVS 180
Db 121 GAAGATSLCFVYPLDFARTLADVCKAGAREFRGIGDCLVYIKSDGKIGLYOGFNVS 180

QY 181 VOGIIIRAAVFGIYDTAKGMLPDPKNTIIVISWMIAGTYAVAGLTSYFDTVRRMM 240
181 VOGIIIRAAVFGIYDTAKGMLPDPKNTIIVISWMIAGTYAVAGLTSYFDTVRRMM 240
Db 181 VOGIIIRAAVFGIYDTAKGMLPDPKNTIIVISWMIAGTYAVAGLTSYFDTVRRMM 240

QY 241 QSGRKGDIWYTGTLDCWKRIARDEGKAFKFGAMSVNLKMGAFVLYLDEIKKY 297
241 QSGRKGDIWYTGTLDCWKRIARDEGKAFKFGAMSVNLKMGAFVLYLDEIKKY 297
Db 241 QSGRKGDIWYTGTLDCWKRIARDEGKAFKFGAMSVNLKMGAFVLYLDEIKKY 297

RESULT 7
ADTL_RAT STANDARD; PRT; 298 AA.

AC 005962;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP, ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
NC NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley, and Wistar; TISSUE-Heart, and Liver;
RX MEDLINE=94002161; PubMed=8399300;
RA Shiohara Y., Kamada M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone encoding rat mitochondrial adenine nucleotide translocator.";
RL Biochim. Biophys. Acta 1152:192-196(1993).
CC CC
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER EXTENT, IN BRAIN AND KIDNEY.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC
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CC
CC EMBL: X61667; CAA3842.1; -
CC EMBL: D12770; BAA0237.1; -
CC PIR: I60173; I60173.
CC InterPro: IPR002067; M1c_carrier.
CC InterPro: IPR002030; M1c_uncoupling.
CC InterPro: IPR001993; M1c_carrier.
CC Pfam: PF00153; mito_carr.3.
CC Rasmussen O.B., Wohlrad H.;
CC PRINTS: PR00926; MITOCARRIER.
CC PRINTS: PR00784; MTUNCOUPLING.

DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32989 MW; 66704FF78C6BC320 CRC64;
Query Match 91.6%; Score 1417; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 3.1e-117;
Matches 266; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTDALSFADFLAGVAAIASTKAVAPIERVKLLQVHASKQITADKQYKGIIDCVR 60
1 MGDQALSFLEDFLAGIAAIVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVR 60
Db 1 MGDQALSFLEDFLAGIAAIVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVR 60

QY 61 IPKEQVLSFWRGNLANVIRFPTQALNFAFKKQYKQIFGVDKRTQFWRPAGNLSG 120
61 IPKEQVLSFWRGNLANVIRFPTQALNFAFKKQYKQIFGVDKRTQFWRPAGNLSG 120
Db 61 IPKEQVLSFWRGNLANVIRFPTQALNFAFKKQYKQIFGVDKRTQFWRPAGNLSG 120

QY 121 GAAGATSLCFVYPLDFARTLADVCKAGAREFRGIGDCLVYIKSDGKIGLYOGFNVS 180
121 GAAGATSLCFVYPLDFARTLADVCKAGAREFRGIGDCLVYIKSDGKIGLYOGFNVS 180
Db 121 GAAGATSLCFVYPLDFARTLADVCKAGAREFRGIGDCLVYIKSDGKIGLYOGFNVS 180

QY 181 VOGIIIRAAVFGIYDTAKGMLPDPKNTIIVISWMIAGTYAVAGLTSYFDTVRRMM 240
181 VOGIIIRAAVFGIYDTAKGMLPDPKNTIIVISWMIAGTYAVAGLTSYFDTVRRMM 240
Db 181 VOGIIIRAAVFGIYDTAKGMLPDPKNTIIVISWMIAGTYAVAGLTSYFDTVRRMM 240

QY 241 QSGRKGDIWYTGTLDCWKRIARDEGKAFKFGAMSVNLKMGAFVLYLDEIKKY 297
241 QSGRKGDIWYTGTLDCWKRIARDEGKAFKFGAMSVNLKMGAFVLYLDEIKKY 297
Db 241 QSGRKGDIWYTGTLDCWKRIARDEGKAFKFGAMSVNLKMGAFVLYLDEIKKY 297

RESULT 8
ADTL_BOVIN STANDARD; PRT; 297 AA.

AC P02722;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP, ATP carrier protein, heart isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
NC NCBI_TaxID=9913;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=89229093; PubMed=2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed differences in various tissues.";
RL Biochemistry 28:866-873(1989).
RN (2)
RP SEQUENCE.
RX MEDLINE=82188267; PubMed=7076130;
RA Agulla H., Misra D., Eulitz M., Klingenberg M.;
RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondria.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).
RN (3)
RP SEQUENCE OF 207-297 FROM N.A.
RX MEDLINE=86295775; PubMed=3017341;
RA Rasmussen O.B., Wohlrad H.;
RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and

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RT an unusually short 3'-noncoding sequence."
RL Biochem. Biophys. Res. Commun. 138:850-857(1986).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
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CC or send an email to license@isb-sdb.ch).
CC -----
DR EMBL; M13783; AAA30363.1; -
DR EMBL; M24102; AAA30768.1; -
DR PIR; A43646; XMO.
DR InterPro: IPR002067; Mtc_carrier.
DR InterPro: IPR002030; Mtc_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00784; MTDCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family; Methylation.
FT INIT_MET 0 0
FT MOD_RES 1 1 BLOCKED.
FT MOD_RES 51 51 METHYLATION (POTENTIAL).
FT TRANSMEM 11 28 1 (POTENTIAL).
FT TRANSMEM 72 90 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 175 194 4 (POTENTIAL).
FT TRANSMEM 213 230 5 (POTENTIAL).
FT TRANSMEM 272 290 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 207 2.
FT REPEAT 208 297 3.
SQ SEQUENCE 297 AA; 32836 MW; A582D3C4A40AEB48 CRC64;
Query Match 91.4%; Score 1414; DB 1; Length 297;
Best Local Similarity 89.9%; Pred. No. 5,6e-117;
Matches 266; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

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DT 01-OCT-1989 (rel. 12, Created)
DT 01-NOV-1990 (rel. 16, Last sequence update)
DT 15-SEP-2003 (rel. 42, Last annotation update)
DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
DE translocase 1) (adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89236396; PubMed=2541251;
RA "Cohen A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
RT ADP/ATP translocase."
RL J. Mol. Biol. 206:261-280(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89340499; PubMed=2547778;
RA Li R., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,
RA Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;
RT "A human muscle adenine nucleotide translocator gene has four exons,
RT is located on chromosome 4, and is differentially expressed."
RL J. Biol. Chem. 264:13998-14004(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88041149; PubMed=2823266;
RA Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;
RT "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack
RT of a leader peptide, divergence from a fibroblast translocator cDNA,
RT and coevolution with mitochondrial DNA genes."
RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 1-37 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
RN [6]
RP VARIANTS PRO-114 AND MET-289.
RX MEDLINE=20385067; PubMed=10926541;
RA Kaukonen J., Jusselius J.K., Tiranli V., Kytälä A., Zeviani M.,
RA Comi G.P., Keranen J., Peltonen L., Suomalainen A.;
RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance."
RL Science 289:782-785(2000).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE

```


CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant
 CC progressive external ophthalmoplegia with various mitochondrial
 CC DNA deletions (PEO). Patients with PEO have mitochondrial
 CC myopathy, progressive external ophthalmoplegia, and other
 CC abnormalities associated with multiple different deletions of
 CC mitochondrial DNA.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC
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 CC
 CC EMBL: J02966; AAA61223.1; -
 CC EMBL: J03593; AAA36751.1; -
 CC EMBL: J04982; AAA51736.1; -
 CC EMBL: BC008664; AA008664.1; -
 CC PIR: A44778; A44778.
 CC Genew: HGNC:10990; SLC25A4.
 CC MIM: 157640; -
 CC MIM: 103220; -
 CC GO: GO:0005887; C:Mitochondrion; TAS.
 CC GO: GO:0005739; C:Mitochondrion; TAS.
 CC GO: GO:0015207; F:adenine transporter activity; TAS.
 CC GO: GO:0006091; P:energy pathways; TAS.
 CC GO: GO:0000002; P:mitochondrial genome maintenance; TAS.
 CC GO: GO:0006832; P:small molecule transport; TAS.
 CC InterPro: IPR002067; M:Mit carrier.
 CC InterPro: IPR002030; M:uncoupling.
 CC InterPro: IPR001993; M:Mitoch-carrier.
 CC Pfam: PF00153; Mito-carrier; 3.
 CC PRINTS: PR00926; MITOCARRIER.
 CC PRINTS: PR00784; MTUNCOUPLING.
 CC PROSITE: PS00215; MITOCH_CARRIER; 3.
 CC DR Mitochondrion; Inner membrane. Repeat; Transmembrane; Transport;
 CC KM Multigene family; Disease mutation.
 CC FT TRANSMEM 12 29 1 (POTENTIAL).
 CC FT TRANSMEM 73 91 2 (POTENTIAL).
 CC FT TRANSMEM 117 134 3 (POTENTIAL).
 CC FT TRANSMEM 176 195 4 (POTENTIAL).
 CC FT TRANSMEM 214 231 5 (POTENTIAL).
 CC FT TRANSMEM 273 291 6 (POTENTIAL).
 CC FT REPEAT 1 110 1.
 CC FT REPEAT 111 208 2.
 CC FT REPEAT 209 298 3.
 CC FT VARIANT 114 114 A -> P (IN PRO).
 CC FT VARIANT 289 289 V -> M (IN PRO).
 CC FT VARIANT 16 16 G -> A (IN REF. 3).
 CC FT CONFLICT 147 149 GCA -> R (IN REF. 3).
 CC FT CONFLICT 227 227 V -> L (IN REF. 3).
 CC SQ SEQUENCE 298 AA; 33064 MW; 59F0DFAC4E7C9B CRC64;
 CC
 CC Query Match 91.38; Score 1413; DB 1; Length 298;
 CC Best Local Similarity 89.24; Pred. No. 6.9e-117;
 CC Matches 265; Conservative 16; Mismatches 16; Indels 0; Gaps 0;
 CC
 CC 1 MTDALSPAKDFLAGGAAIASTKTAAPTEKVLLOVQASQIADKQYKIIICVYR 60
 CC 1 MGDAHSFLKDFLAGGAAIAVSTKTAAPTEKVLLOVQASQIADKQYKIIICVYR 60
 CC 1 IPKEQVLSFWKGNLANVIRYPTQALNFAFKDKYKQIIFGVDKRTQFWRYAGNLIASG 120
 CC 61 IPKEQVLSFWKGNLANVIRYPTQALNFAFKDKYKQIIFGVDKRTQFWRYAGNLIASG 120
 CC 61 IPKEQVLSFWKGNLANVIRYPTQALNFAFKDKYKQIIFGVDKRTQFWRYAGNLIASG 120

QY 121 GAAGATSLCFVYPLDFARTRLADYKAGAREFERGLGDLVYKNSDGKLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADYKAGAREFERGLGDLVYKNSDGKLYOGFNVS 180
 QY 181 VGGIIIRYAAFEIYOTAKGMDPKNTHTVISMIAQYTVAVAGLTSPEDTVRRMMK 240
 DB 181 VGGIIIRYAAFEIYOTAKGMDPKNTHTVISMIAQYTVAVAGLTSPEDTVRRMMK 240
 QY 241 QSGRKGDIMYTGTLDCWKRIARDEGKAFKFAKAWSNVLRMGAGAVLYLDEIKKY 297
 DB 241 QSGRKGDIMYTGTLDCWKRIARDEGKAFKFAKAWSNVLRMGAGAVLYLDEIKKY 297
 RESULT 10
 ADT_DROME STANDARD; PRT: 299 AA.
 AC Q26365; P91614; Q26254; Q95530; Q9VZ70;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADP/ATP carrier protein (ADP/ATP translocase) (adenine nucleotide
 DE translocator) (ANT) (Stress sensitive B protein).
 GN SCSB OR A/R-T OR CG16944.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID:7227;
 RX MEDLINE-92389367; PubMed-1387687;
 RT Louvi A., Tsitilon S.G.;
 RT "A cDNA clone encoding the ADP/ATP translocase of Drosophila
 RT melanogaster shows a high degree of similarity with the mammalian
 RT ADP/ATP translocases";
 RL J. Mol. Evol. 35:44-50(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-94350065; PubMed-7520869;
 RT Hutter P., Karch F.;
 RT "Molecular analysis of a candidate gene for the reproductive
 RT isolation between sibling species of Drosophila";
 RL Experientia 50:749-762(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN-Oregon-R;
 RA Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburner M.;
 RN Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Berkeley;
 RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Neilson C.R., Miklos G.L.G.,
 RA Abril J.F., Abmayyan A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokhov D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burris K.C., Busam D.A., Butler C., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de la Piedad B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

FT TRANSMEM 178 197 4 (POTENTIAL).
 FT TRANSMEM 216 233 5 (POTENTIAL).
 FT TRANSMEM 275 293 6 (POTENTIAL).
 SQ SEQUENCE 301 AA; 32863 MW; 4CC9E17C9F8DA08B CRC64;

Query Match
 Best Local Similarity 76.9%; Score 1190; DB 1; Length 301;
 Matches 227; Conservative 18; Mismatches 43; Indels 0; Gaps 0;

8 FANDELAGVAAAIKSTAVAPIERVKLLQVQHSKQITADKQYKGIIDCVIRPKQEV 67
 10 FANDELAGGISAASVSKAVAPIERVKLLQVQAAKIAADKQYKGIIDCVIRPKQGI 69
 DB
 QY 68 LSTFRGRLANVIRFPQALNFAFKKQYKQIFLGVDKRTQFVRFAAGNLASGAGATS 127
 70 GAWRGMLANVIRFPQALNFAFKKQYKQIFLGVDKRTQFVRFAAGNLASGAGATS 129
 DB
 QY 128 LCFEYPLDFAFRTLAADVAGKAGAEFRFGIDGLVKYKSDGKIGLYOGFNVSVQGITIY 187
 130 LCFEYPLDFAFRTLAADVAGKAGAEFRFGIDGLVKYKSDGKIGLYOGFNVSVQGITIY 189
 DB
 QY 188 RAAVFGIYDTAKGMLPDKNTHTVISMIAQVTAVAGLTSYFEDTVRRMMQSGRGT 247
 190 RAAVFGCEFDKAGMLPDKNTHTVISMIAQVTAVAGLTSYFEDTVRRMMQSGRGT 249
 DB
 QY 248 DIWYTGILDCWKRIARDEGKAFKGAWSNVLRGAGAFVLYLDEIKY 295
 250 EWMYKNTLDCWKRIARDEGKAFKGAWSNVLRGAGAFVLYLDEIKY 297
 DB

RESULT 12
 ADT_CHLKE
 ID ADT_CHLKE STANDARD; PRT; 339 AA.

AC F31692;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE ADP,ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).
 OS Chlorocella kessleri.
 OS Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales; Chlorellaceae; Chlorocella.
 OC NCBI_TaxID=3074;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92084708; PubMed=1748677;
 RA Hilgath C., Sauer N., Tanner W.;
 RT "Glucose increases the expression of the ATP/ADP translocator and the glyceraldehyde-3-phosphate dehydrogenase genes in Chlorocella.";
 RL J. Biol. Chem. 266:24044-24047(1991).
 CC
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC
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 CC
 CC EMBL: M76669; AAA3027.1; -
 CC PIR: A41677; A41677.
 CC InterPro: IPR002067; Mlt_carrier.
 CC InterPro: IPR001993; MitoCh_carrier.
 CC Pfam: PF00153; mltocarr; 3.
 CC PRINTS: PR00926; MITOCARRIER.
 CC PROSITE: PS00215; MITOCH_CARRIER; 3.

KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 45 62 1 (POTENTIAL).
 FT TRANSMEM 108 126 2 (POTENTIAL).
 FT TRANSMEM 151 168 3 (POTENTIAL).
 FT TRANSMEM 209 228 4 (POTENTIAL).
 FT TRANSMEM 248 265 5 (POTENTIAL).
 FT TRANSMEM 304 322 6 (POTENTIAL).
 SQ SEQUENCE 339 AA; 36686 MW; 54779734A33B3942 CRC64;

Query Match
 Best Local Similarity 62.6%; Score 968; DB 1; Length 339;
 Matches 194; Conservative 29; Mismatches 64; Indels 8; Gaps 5;

6 LSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHSKQITADK--QYKGIIDCVIRPK 63
 39 MAEYKDLLAGGTAISAISKTAAPIERVKLLQVQDSNPMKISGQVPRYTIVNCFRVSS 98
 DB
 QY 64 EGVLSFRGRNLNANVIRFPQALNFAFKKQYKQIFLGVDKRTQFVRFAAGNLASGAA 123
 66 EGVLSFRGRNLNANVIRFPQALNFAFKKQYKQIFLGVDKRTQFVRFAAGNLASGAA 125
 DB
 QY 99 EGVASFWRNLNANVIRFPQALNFAFKKQYKQIFLGVDKRTQFVRFAAGNLASGAA 157
 124 GATSLCFEYPLDFAFRTLAADVAGKAGAEFRFGIDGLVKYKSDGKIGLYOGFNVSVQ 183
 158 GAGSLILVYPLDFAFRTLAADVAG--SGKSRFETGLVDLSKRVYRGPMALYQGFVSQ 216
 DB
 QY 184 IIVYRAVFGIYDTAKGML-PDKNTHTVISMIAQVTAVAGLTSYFEDTVRRMMQSG 242
 217 IIVYRGAVFGIYDTAKGML-PDKNTHTVISMIAQVTAVAGLTSYFEDTVRRMMQSG 249
 DB
 QY 243 GRKGTDMYTGILDCWKRIARDEGKAFKGAWSNVLRGAGAFVLYLDEIKY 297
 277 --GGRQYNGTIDCWKRKVAQDQGMKAFKGAWSNVLRGAGAFVLYLDEIKY 328
 DB

RESULT 13
 ADT1_GOSHI
 ID ADT1_GOSHI STANDARD; PRT; 386 AA.

AC 022342;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADP,ATP carrier protein 1, mitochondrial precursor (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
 OS Gossypium hirsutum (Upland cotton).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
 OC NCBI_TaxID=3635;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Texas Marker 1; TISSUE=Fiber;
 RA Shih H., Brown R.M. Jr.;
 RT "Two cDNA sequences for the adenine nucleotide translocator, CANT1 and CANT2, from cotton fibers (Gossypium hirsutum)." ;
 RL (in) Plant Gene Register PGR97-130.
 CC
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC
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 CC
 CC EMBL: AF006489; AAB72047.1; -
 CC PIR: T09709; T09709.
 CC InterPro: IPR002067; Mlt_carrier.
 CC InterPro: IPR001993; MitoCh_carrier.
 CC Pfam: PF00153; mltocarr; 3.

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DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Transit peptide; Multigene family.
FT TRANSIT 1 76 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 77 386 ADP/ATP CARRIER PROTEIN 1.
FT TRANSMEM 90 107 1 (POTENTIAL).
FT TRANSMEM 152 170 2 (POTENTIAL).
FT TRANSMEM 195 212 3 (POTENTIAL).
FT TRANSMEM 256 275 4 (POTENTIAL).
FT TRANSMEM 295 312 5 (POTENTIAL).
FT TRANSMEM 351 369 6 (POTENTIAL).
SQ SEQUENCE 386 AA; 42093 MW; A05F6C73EEDEE6 CRC64;

Query Match 49.8%; Score 771; DB 1; Length 386;
Best Local Similarity 55.4%; Pred. No. 2.3e-60;
Matches 169; Conservative 35; Mismatches 79; Indels 22; Gaps 7;

OY 7 SPANFLAGVAAIAISKTAAPIERKLLIOVQ-HASKQTADKQYKGIIDCVRIPEQ 65
DB 85 SFADFLMGVSAVSKTAAPIERKLLIONODEMIRSGRLSEYKIGICGCFRTIDE 144
OY 66 EVLSFWRGNTANVIRYPTQALNFAKDKYKQIFLGVDKRTQFWRYFAGNLASGAGA 125
DB 145 GFGSLMRGNTANVIRYPTQALNFAKDKYKQIFLGVDKRTQFWRYFAGNLASGAGA 203
OY 126 TSLCFVYPLDPAFRLADV-VGKAGAREFERGLDCLVTKYKSDIGIKGLYOGFNVSYG 183
DB 204 SSLFVYSLDPAFRLADVAAKKGGEROGLVDYRKLKSGINGLVRGFIISCVG 263
OY 184 IITRAAFVGIYDPAK-----GMLPDKNTNIVISWMTAQVTVAVAGLTSPEFTVRRM 238
DB 264 IIVRGVLFEGMDSLKPVLTGSMODSFFASVFLGMLT-----TNGAALASYPIDVRRRM 319
OY 239 MMOSGRKTDIMYGTGLCMRKIRADEGKAFEGKAGWENYLRGMGAFVLYLDEI---- 294
DB 320 MMTSGKA---VKYSSLDPAFSGIILNKGKSLFKGAGSNILNALAGVLAGYDKQLIV 376
OY 295 --KKY 297
DB 377 FGKKY 381

RESULT 14
ADT_SCHPO STANDARD: PRT: 322 AA.
AC 009188:
DT 01-NOV-1997 (Rel. 35, last sequence update)
DT 28-FEB-2003 (Rel. 41, last annotation update)
DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
translocator) (ANT).
GN ANCI OR SPBC530.10C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=96257204; PubMed=8675018;
RA Couzin N., Trezeguet V., Saux A.L., Lauguin G.J.M.;
RT Cloning of the gene encoding the mitochondrial adenine nucleotide
carrier of Schizosaccharomyces pombe by functional complementation in
RT Saccharomyces cerevisiae.
RL Gene 171:113-117(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

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RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gellies S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy U., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,
RA Weljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Mambutt R., Purrelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Talada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
RA "The genome sequence of Schizosaccharomyces pombe."
RT Nature 415:871-880(2002).
CC - FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC - SUBUNIT: Homodimer (By similarity).
CC - SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC - DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC - SIMILARITY: Belongs to the mitochondrial carrier family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL: 249974; CA90275.1; -.
DR EMBL: AL023634; CA91976.1; -.
DR PIR: T40526; T40526.
DR GeneDB: SPombe; SPBC530.10C; -.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001963; Mitoch_carrier.
DR Pfam: PR00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 28 48 1 (POTENTIAL).
FT TRANSMEM 93 111 2 (POTENTIAL).
FT TRANSMEM 131 151 3 (POTENTIAL).
FT TRANSMEM 197 217 4 (POTENTIAL).
FT TRANSMEM 222 242 5 (POTENTIAL).
FT TRANSMEM 289 309 6 (POTENTIAL).
SQ SEQUENCE 322 AA; 35020 MW; 8AC3D16A40F41AFC CRC64;

Query Match 49.8%; Score 770; DB 1; Length 322;
Best Local Similarity 53.6%; Pred. No. 2.3e-60;
Matches 158; Conservative 51; Mismatches 74; Indels 12; Gaps 6;

OY 7 SPANFLAGVAAIAISKTAAPIERKLLIOVQ-HASKQTADKQYKGIIDCVRIPEK 63
DB 26 TFFPDMGVSAAVSKTAAPIERKLLIONQ--DEMIRAGLSIRYKIGEGCFRTAA 83
OY 64 EVLSFWRGNTANVIRYPTQALNFAKDKYKQIFLGVDKRTQFWRYFAGNLASGAGA 123
DB 84 EGVLSIMRGNTANVIRYPTQALNFAKDKYKQIFLGVDKRTQFWRYFAGNLASGAGA 142
OY 124 GATSLCFVYPLDPAFRLADV--GKAGAREFERGLDCLVTKYKSDIGIKGLYOGFNVSY 181
DB 143 GASLLEFVYSLDPAFRLADVAAKKGGEROGLVDYRKLKSGINGLVRGFIISCV 202

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Db      121 GAAGATSLCFVYPLDPAKRLADVGKAGEREFGDGLVITYSDGRLGYOGFNVS 180
QY      181 VGGIITIRAAVFGIYDTAKGMLPDPKNTHTIVISMTAQVTAVAGLTSYFPTVRRMM 240
Db      181 VGGIITIRAAVFGIYDTAKGMLPDPKNTHTIVISMTAQVTAVAGLTSYFPTVRRMM 240
QY      241 QSGRKGTDMYTGTLDCWKRIADDEGKAFKFGKAMSNVLRGMGAVLVLYDEIKRYT 298
Db      241 QSGRKGTDMYTGTLDCWKRIADDEGKAFKFGKAMSNVLRGMGAVLVLYDEIKRYT 298

RESULT 2
O9PRH10 PRELIMINARY; PRT; 298 AA.
AC O8JH10;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Solute carrier family 25 member 5 protein.
GN SLC25A5.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22035902; PubMed=12006978;
RA Gollig G., Amsterdam A., Sun Z., Antonelli M., Maldonado E., Chen W.,
RA Burgess S., Haldt M., Artzt K., Farrington S., Lin S.-Y., Nissen R.M.,
RA Hopkins N.;
RT "Insertional mutagenesis in zebrafish rapidly identifies genes
RT essential for early vertebrate development."
RL Nat. Genet. 31:135-140(2002).
DR EMBL: AF506216; AAM34660.1; -
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR Pfam: PF00153; mito_car1; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
SQ SEQUENCE 298 AA; 32763 MW; D78663CF65C51D39 CRC64;

Query Match 93.7%; Score 1450; DB 13; Length 298;
Best Local Similarity 92.9%; Pred. No. 3e-120;
Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTDAAISFAKDFLAGVAAAISTKTAAPIERVKLLIQVOHASKQITADKOYKGIIDCVVR 60
Db 1 MTDAAISFAKDFLAGVAAAISTKTAAPIERVKLLIQVOHASKQITADKOYKGIIDCVVR 60
QY 1 MTDAAISFAKDFLAGVAAAISTKTAAPIERVKLLIQVOHASKQITADKOYKGIIDCVVR 60
Db 1 MTDAAISFAKDFLAGVAAAISTKTAAPIERVKLLIQVOHASKQITADKOYKGIIDCVVR 60
QY 61 IPKEQEVLSFWKGNLANVIRYPTQALNFAFKDKYQIFLGVGDKRTQFWRVAGNVLASG 120
Db 61 IPKEQEVLSFWKGNLANVIRYPTQALNFAFKDKYQIFLGVGDKRTQFWRVAGNVLASG 120
QY 121 GAAGATSLCFVYPLDPAKRLADVGKAGEREFGDGLVITYSDGRLGYOGFNVS 180
Db 121 GAAGATSLCFVYPLDPAKRLADVGKAGEREFGDGLVITYSDGRLGYOGFNVS 180
QY 181 VGGIITIRAAVFGIYDTAKGMLPDPKNTHTIVISMTAQVTAVAGLTSYFPTVRRMM 240
Db 181 VGGIITIRAAVFGIYDTAKGMLPDPKNTHTIVISMTAQVTAVAGLTSYFPTVRRMM 240
QY 241 QSGRKGTDMYTGTLDCWKRIADDEGKAFKFGKAMSNVLRGMGAVLVLYDEIKRYT 296
Db 241 QSGRKGTDMYTGTLDCWKRIADDEGKAFKFGKAMSNVLRGMGAVLVLYDEIKRYT 296

RESULT 3
O9PRH1 PRELIMINARY; PRT; 298 AA.

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AC O9PRH1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (winkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ontani H., Nakamura M., Ichikawa Y., Satoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT Z, W, X, and Y in the frog Rana rugosa. Inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1-SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB008463; BAA36513.1; -
DR EMBL: AB008456; BAA36506.1; -
DR EMBL: AB008461; BAA36511.1; -
DR EMBL: AB008462; BAA36512.1; -
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR Pfam: PF00153; mito_car1; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;

Query Match 93.5%; Score 1446; DB 13; Length 298;
Best Local Similarity 91.9%; Pred. No. 6.8e-120;
Matches 273; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTDAAISFAKDFLAGVAAAISTKTAAPIERVKLLIQVOHASKQITADKOYKGIIDCVVR 60
Db 1 MTDAAISFAKDFLAGVAAAISTKTAAPIERVKLLIQVOHASKQITADKOYKGIIDCVVR 60
QY 1 MTDAAISFAKDFLAGVAAAISTKTAAPIERVKLLIQVOHASKQITADKOYKGIIDCVVR 60
Db 1 MTDAAISFAKDFLAGVAAAISTKTAAPIERVKLLIQVOHASKQITADKOYKGIIDCVVR 60
QY 61 IPKEQEVLSFWKGNLANVIRYPTQALNFAFKDKYQIFLGVGDKRTQFWRVAGNVLASG 120
Db 61 IPKEQEVLSFWKGNLANVIRYPTQALNFAFKDKYQIFLGVGDKRTQFWRVAGNVLASG 120
QY 121 GAAGATSLCFVYPLDPAKRLADVGKAGEREFGDGLVITYSDGRLGYOGFNVS 180
Db 121 GAAGATSLCFVYPLDPAKRLADVGKAGEREFGDGLVITYSDGRLGYOGFNVS 180
QY 181 VGGIITIRAAVFGIYDTAKGMLPDPKNTHTIVISMTAQVTAVAGLTSYFPTVRRMM 240
Db 181 VGGIITIRAAVFGIYDTAKGMLPDPKNTHTIVISMTAQVTAVAGLTSYFPTVRRMM 240
QY 241 QSGRKGTDMYTGTLDCWKRIADDEGKAFKFGKAMSNVLRGMGAVLVLYDEIKRYT 297
Db 241 QSGRKGTDMYTGTLDCWKRIADDEGKAFKFGKAMSNVLRGMGAVLVLYDEIKRYT 297

RESULT 4
O9PRH2 PRELIMINARY; PRT; 298 AA.
AC O9PRH2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (winkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ontani H., Nakamura M., Ichikawa Y., Satoh K.;

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"The origin and differentiation of the heteromorphic sex chromosomes of 2, W, X, and Y in the frog *Rana rugosa*, inferred from the sequences of a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB008460; BAA36510.1; -;
 DR EMBL: AB008458; BAA36508.1; -;
 DR EMBL: AB008459; BAA36509.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00784; MITOCH_CARRIER; 3.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Membrane; Transmembrane; Transport.
 SO SEQUENCE 298 AA; 33082 MW; BOE225E867599A06 CRC64;

Query Match 93.3%; Score 1443; DB 13; Length 298;
 Best Local Similarity 91.6%; Pred. No. 1.2e-119;
 Matches 272; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

OY 1 MTDAALSPAKDFLAGVAAAIKTAIVAPIERVKLLIQVHASKOTADKQYKGIIDCYVR 60
 DB 1 MTDAALSPAKDFLAGVAAAIKTAIVAPIERVKLLIQVHASKOTADKQYKGIIDCYVR 60
 OY 61 IPKEDEVLSFWGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
 DB 61 IPKEDEVLSFWGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
 OY 121 GAAGATSLCFYPLDFARTRLADYGVKAGAREFERGLDCLVKIKYKSGIKGLYOGFNVS 180
 DB 121 GAAGATSLCFYPLDFARTRLADYGVKAGAREFERGLDCLVKIKYKSGIKGLYOGFNVS 180
 OY 181 VGGIIYRAAFYGIYDFAKGMPLDPKRNTHIVSMIAQTVAVAGILTSYPTVRRMM 240
 DB 181 VGGIIYRAAFYGIYDFAKGMPLDPKRNTHIVSMIAQTVAVAGILTSYPTVRRMM 240
 OY 241 QSGRKGDTIMYTGTLDCWRKRIARDEGSAFFKGAWSNVLRGMGAFVLYLDEIKKY 297
 DB 241 QSGRKGDTIMYTGTLDCWRKRIARDEGSAFFKGAWSNVLRGMGAFVLYLDEIKKY 297
 RESULT 5
 OYAC 08AYM3 PRELIMINARY; PRT; 298 AA.
 AC 08AYM3:
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE ATP/ADP antiporter.
 GN AVANT.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba Y.;
 RT "Cold-induced mitochondrial uncoupling and expression of chicken UCP
 RT and ANT mRNA in chicken skeletal muscle.";
 RL FEBS Lett. 0:0-0(2002).
 DR EMBL: AB088686; BAC15533.1; -;
 SO SEQUENCE 298 AA; 32847 MW; 1174C05EC400A10D CRC64;

Query Match 93.3%; Score 1443; DB 13; Length 298;
 Best Local Similarity 92.9%; Pred. No. 1.2e-119;
 Matches 275; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

OY 1 MTDAALSPAKDFLAGVAAAIKTAIVAPIERVKLLIQVHASKOTADKQYKGIIDCYVR 60
 DB 1 MADAALSPKDFLAGVAAAIKTAIVAPIERVKLLIQVHASKOTADKQYKGIIDCYVR 60

OY 61 IPKEDEVLSFWGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
 DB 61 IPKEDEVLSFWGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
 OY 121 GAAGATSLCFYPLDFARTRLADYGVKAGAREFERGLDCLVKIKYKSGIKGLYOGFNVS 180
 DB 121 GAAGATSLCFYPLDFARTRLADYGVKAGAREFERGLDCLVKIKYKSGIKGLYOGFNVS 180
 OY 181 VGGIIYRAAFYGIYDFAKGMPLDPKRNTHIVSMIAQTVAVAGILTSYPTVRRMM 240
 DB 181 VGGIIYRAAFYGIYDFAKGMPLDPKRNTHIVSMIAQTVAVAGILTSYPTVRRMM 240
 OY 241 QSGRKGDTIMYTGTLDCWRKRIARDEGSAFFKGAWSNVLRGMGAFVLYLDEIKKY 296
 DB 241 QSGRKGDTIMYTGTLDCWRKRIARDEGSAFFKGAWSNVLRGMGAFVLYLDEIKKY 296

Query Match 93.0%; Score 1439; DB 13; Length 298;
 Best Local Similarity 91.2%; Pred. No. 2.8e-119;
 Matches 271; Conservative 16; Mismatches 10; Indels 0; Gaps 0;

OYAC 09YIC4 PRELIMINARY; PRT; 298 AA.
 AC 09YIC4:
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS *Rana rugosa* (Fringed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; *Rana*.
 OX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99083429; PubMed-9866197;
 RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Satoh K.;
 RT "The origin and differentiation of the heteromorphic sex chromosomes of 2, W, X, and Y in the frog *Rana rugosa*, inferred from the sequences of a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB008457; BAA36507.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MITOCH_CARRIER; 3.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Membrane; Transmembrane; Transport.
 SO SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;

Query Match 93.0%; Score 1439; DB 13; Length 298;
 Best Local Similarity 91.2%; Pred. No. 2.8e-119;
 Matches 271; Conservative 16; Mismatches 10; Indels 0; Gaps 0;

OY 1 MTDAALSPAKDFLAGVAAAIKTAIVAPIERVKLLIQVHASKOTADKQYKGIIDCYVR 60
 DB 1 MADAALSPKDFLAGVAAAIKTAIVAPIERVKLLIQVHASKOTADKQYKGIIDCYVR 60
 OY 61 IPKEDEVLSFWGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
 DB 61 IPKEDEVLSFWGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
 OY 121 GAAGATSLCFYPLDFARTRLADYGVKAGAREFERGLDCLVKIKYKSGIKGLYOGFNVS 180
 DB 121 GAAGATSLCFYPLDFARTRLADYGVKAGAREFERGLDCLVKIKYKSGIKGLYOGFNVS 180
 OY 181 VGGIIYRAAFYGIYDFAKGMPLDPKRNTHIVSMIAQTVAVAGILTSYPTVRRMM 240
 DB 181 VGGIIYRAAFYGIYDFAKGMPLDPKRNTHIVSMIAQTVAVAGILTSYPTVRRMM 240
 OY 241 QSGRKGDTIMYTGTLDCWRKRIARDEGSAFFKGAWSNVLRGMGAFVLYLDEIKKY 297
 DB 241 QSGRKGDTIMYTGTLDCWRKRIARDEGSAFFKGAWSNVLRGMGAFVLYLDEIKKY 297


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RESULT 7
0919M9
ID 0919M9 PRELIMINARY; PRT; 298 AA.
AC 0919M9;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Adenine nucleotide translocase.
GN ANTL.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Crawford M.J., Khosrowshahian F., Varmuza S.L., Liversage R.A.;
RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
RT Dynamic Patterns of Expression During Development."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL: AF23147; AAF63471.1; -.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR pfam: PF00153; Mitoc_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00784; MTUNCOUPLING.
DR MEMBRANE: TRANSMEMBRANE; TRANSPORT.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 32940 MW; 91B740133751877E CRC64;

Query Match 92.1%; Score 1425; DB 13; Length 298;
Best Local Similarity 91.6%; Pred. No. 4,9e-118;
Matches 271; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTDAISPAKDFLAGVAAAIKSTVAAPIERVKLLQOVHASKQITADKQYKGIIDCVR 60
DB 1 MTDAISPAKDFLAGVAAAIKSTVAAPIERVKLLQOVHASKQITADKQYKGIIDCVR 60
QY 61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKRTQFRRYFAGNLASG 120
DB 61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKRTQFRRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLADAVGKAGAREFERGLDCLVYIKSDGKIGLYOGFNVS 180
DB 121 GAAGATSLCFVYPLDFARTLADAVGKAGAREFERGLDCLVYIKSDGKIGLYOGFNVS 180
QY 181 VGGIIYRAAYFGIYDTAKGMLDPKNTHTIVSMIAQVTAAGLTSYFDTVRRRMM 240
DB 181 VGGIIYRAAYFGIYDTAKGMLDPKNTHTIVSMIAQVTAAGLTSYFDTVRRRMM 240
QY 181 VGGIIYRAAYFGIYDTAKGMLDPKNTHTIVSMIAQVTAAGLTSYFDTVRRRMM 240
DB 181 VGGIIYRAAYFGIYDTAKGMLDPKNTHTIVSMIAQVTAAGLTSYFDTVRRRMM 240
QY 241 OSGRKGTIDMYTGLDCKRKRIARDEGKAFFKGAWSNVLRMGAFVLVYDEIKK 296
DB 241 OSGRKGTIDMYTGLDCKRKRIARDEGKAFFKGAWSNVLRMGAFVLVYDEIKK 296
DB 241 OSGRKGTIDMYTGLDCKRKRIARDEGKAFFKGAWSNVLRMGAFVLVYDEIKK 296

RESULT 8
046373
ID 046373 PRELIMINARY; PRT; 298 AA.
AC 046373;
DT 01-JUN-1998 (TEMBLrel. 06, Created)
DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Skeletal muscle;
RA Yamaguchi N., Kasai M.;
RT "Identification of a 30kDa calsequestrin-binding protein, which
RT regulates calcium release from sarcoplasmic reticulum of rabbit
RT skeletal muscle."
RL J. Biochem. 335:541-547(1998).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL: AB009386; BAA23777.1; -.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR pfam: PF00153; Mitoc_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00784; MTUNCOUPLING.
DR MEMBRANE: TRANSMEMBRANE; TRANSPORT.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 32901 MW; CAEA32C88164AD78 CRC64;

Query Match 92.0%; Score 1423; DB 6; Length 298;
Best Local Similarity 89.9%; Pred. No. 7,4e-118;
Matches 267; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTDAISPAKDFLAGVAAAIKSTVAAPIERVKLLQOVHASKQITADKQYKGIIDCVR 60
DB 1 MSDQALSLKDFLAGVAAAVSTVAAPIERVKLLQOVHASKQITADKQYKGIIDCVR 60
QY 61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKRTQFRRYFAGNLASG 120
DB 61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKRTQFRRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLADAVGKAGAREFERGLDCLVYIKSDGKIGLYOGFNVS 180
DB 121 GAAGATSLCFVYPLDFARTLADAVGKAGAREFERGLDCLVYIKSDGKIGLYOGFNVS 180
QY 181 VGGIIYRAAYFGIYDTAKGMLDPKNTHTIVSMIAQVTAAGLTSYFDTVRRRMM 240
DB 181 VGGIIYRAAYFGIYDTAKGMLDPKNTHTIVSMIAQVTAAGLTSYFDTVRRRMM 240
QY 241 OSGRKGTIDMYTGLDCKRKRIARDEGKAFFKGAWSNVLRMGAFVLVYDEIKK 297
DB 241 OSGRKGTIDMYTGLDCKRKRIARDEGKAFFKGAWSNVLRMGAFVLVYDEIKK 297

RESULT 9
08BV19
ID 08BV19 PRELIMINARY; PRT; 298 AA.
AC 08BV19;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Solute carrier family 25.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognath; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; Pubmed=12466851;
RA THE FANTOM Consortium.
RA THE RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT Nature 420:563-573(2002).
DR EMBL: AK078077; BAC37117.1; -.
SQ SEQUENCE 298 AA; 32904 MW; F94C89009836710B CRC64;

Query Match 91.6%; Score 1417; DB 11; Length 298;
Best Local Similarity 89.6%; Pred. No. 2,5e-117;
Matches 266; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTDAISPAKDFLAGVAAAIKSTVAAPIERVKLLQOVHASKQITADKQYKGIIDCVR 60
DB 1 MTDAISPAKDFLAGVAAAIKSTVAAPIERVKLLQOVHASKQITADKQYKGIIDCVR 60

```


DB 129 TSLCFVYPLDPAFRLADTGK-GGQREFTGLGNCLAIKFSKSDGLVGLRGFVSVGGII 187
 QY 186 IYRAAFEGIDYPAKMLDPKRNTHIVISMIAQVTAAGLTSYDFDVRRRMMQSGRK 245
 DB 188 IYRAAFEGIDYPAKMLDPKRNTHIVISMIAQVTAAGLTSYDFDVRRRMMQSGRK 247
 QY 246 GTDITMTGTLDCWKRIARDEGKAFFKGAWSNVLKMGAFVLYLDEIKKY 297
 DB 248 ATEIIYKNTLHCWATIAKOEIGAFKGAWSNVLKMGAFVLYLDEIKKY 299

RESULT 14

044093 PRELIMINARY: PRT; 288 AA.
 ID 044093
 AC 044093;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE ADP/ATP translocase (Fragment).
 GN SESB.
 OS Drosophila pseudoobscura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 CC Ephydroidea; Drosophilidae; Drosophila.
 RX NCBI_TaxID=7237;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
 RL Genetics 0:0-0(1997).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AF025799; AAB87884.1; -.
 DR Flybase; FBgn0023292; Dpse\sesb.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR Membrane; Repeat; Transmembrane; Transport.
 KW NON_TER 288
 FT
 SQ SEQUENCE 288 AA; 31725 MW; 052B0CC0050436B0 CRC64;

Query Match 77.0%; Score 1190.5; DB 5; Length 288;
 Best Local Similarity 80.4%; Pred. No. 2.8e-97;
 Matches 229; Conservative 20; Mismatches 33; Indels 3; Gaps 3;

QY 5 ALSFAKDLFAGVAAAIKSTAVAPIERVKLLQVOHASQITADKOYKGIIDCVRIPE 64
 DB 7 AIGFVKDPAAGGISAASVSTAVAPIERVKLLQVOHISKQISPDKQKGMVDCFTIRIPE 66
 QY 65 QEVLSFWRGNTLVNIRYFPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLAGSGAAG 124
 DB 67 QGFSSFWRGNTLVNIRYFPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLAGSGAAG 126
 QY 125 ATSLCFVYPLDPAFRLADVGKAGAREFRGLDCLVKIYKSDGKIGLYGFNVSVGCI 184
 DB 127 ATSLCFVYPLDPAFRLADVGKAGAREFRGLDCLVKIYKSDGKIGLYGFNVSVGCI 185
 QY 185 IYRAAFEGIDYPAKMLDPKRNTHIVISMIAQVTAAGLTSYDFDVRRRMMQSGR 244
 DB 186 IYRAAFEGIDYPAKMLDPKRNTHIVISMIAQVTAAGLTSYDFDVRRRMMQSGR 244
 QY 245 KGTDIYMTGTLDCWKRIARDEGKAFFKGAWSNVLKMGAFVLY 289
 DB 245 KATEIIYKNTLHCWATIAKOE-GSAFFKGAWSNVLKMGAFVLY 288

RESULT 15

044094 PRELIMINARY: PRT; 288 AA.
 ID 044094
 AC 044094;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE ADP/ATP translocase (Fragment).
 GN SESB.
 OS Drosophila subobscura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 CC Ephydroidea; Drosophilidae; Drosophila.
 RX NCBI_TaxID=7241;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
 RL Genetics 0:0-0(1997).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AF025799; AAB87884.1; -.
 DR Flybase; FBgn0023292; Dpse\sesb.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR Membrane; Repeat; Transmembrane; Transport.
 KW NON_TER 288
 FT
 SQ SEQUENCE 288 AA; 31775 MW; 06A1D1E477E81B26 CRC64;

Query Match 76.6%; Score 1185.5; DB 5; Length 288;
 Best Local Similarity 80.0%; Pred. No. 7.7e-97;
 Matches 228; Conservative 21; Mismatches 33; Indels 3; Gaps 3;

QY 5 ALSFAKDLFAGVAAAIKSTAVAPIERVKLLQVOHASQITADKOYKGIIDCVRIPE 64
 DB 7 AIGFVKDPAAGGISAASVSTAVAPIERVKLLQVOHISKQISPDKQKGMVDCFTIRIPE 66
 QY 65 QEVLSFWRGNTLVNIRYFPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLAGSGAAG 124
 DB 67 QGFSSFWRGNTLVNIRYFPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLAGSGAAG 126
 QY 125 ATSLCFVYPLDPAFRLADVGKAGAREFRGLDCLVKIYKSDGKIGLYGFNVSVGCI 184
 DB 127 ATSLCFVYPLDPAFRLADVGKAGAREFRGLDCLVKIYKSDGKIGLYGFNVSVGCI 185
 QY 185 IYRAAFEGIDYPAKMLDPKRNTHIVISMIAQVTAAGLTSYDFDVRRRMMQSGR 244
 DB 186 IYRAAFEGIDYPAKMLDPKRNTHIVISMIAQVTAAGLTSYDFDVRRRMMQSGR 244
 QY 245 KGTDIYMTGTLDCWKRIARDEGKAFFKGAWSNVLKMGAFVLY 289
 DB 245 KATEIIYKNTLHCWATIAKOE-GTAFKGAWSNVLKMGAFVLY 288

Search completed: August 28, 2003, 19:42:10
 Job time : 51.3897 secs

PA (MITO-) MITOKOR.
 XX
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 XX
 DR WPI: 2000-365619/31.
 DR N-PSDB: AAD00521.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 PS Claim 46: Page 173-174; 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MLAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MID), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT3 from human brain.
 CC
 XX
 SQ Sequence 298 AA;
 Query Match 100.0%; Score 1543; DB 21; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4, 6e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTEQAIISPAKDFLAGGIAAIAISKTAAPIERVKLLQVOHASKQIADKQKGIYDCIYR 60
 DB 1 MTEQAIISPAKDFLAGGIAAIAISKTAAPIERVKLLQVOHASKQIADKQKGIYDCIYR 60
 QY 61 IPEQGVLSFWKGNLANVIRYPTQALNFAFKDKYQKIFLGVDKHTQFWRYFAGNLAGS 120
 DB 61 IPEQGVLSFWKGNLANVIRYPTQALNFAFKDKYQKIFLGVDKHTQFWRYFAGNLAGS 120
 QY 121 GAAGATSLCFVYPLDPAFRTRLADVGKSGTEREFGDGLVYKITSDDGIRGLYQGFVS 180
 DB 121 GAAGATSLCFVYPLDPAFRTRLADVGKSGTEREFGDGLVYKITSDDGIRGLYQGFVS 180
 QY 181 VGGIITIRAAFGVYDTAKGMLPDPKNTHTIVSWMTAQTVTAAGVSYPPDTRRRMM 240
 DB 181 VGGIITIRAAFGVYDTAKGMLPDPKNTHTIVSWMTAQTVTAAGVSYPPDTRRRMM 240
 QY 241 QSGRGADIMYGTVCWKRIEFDGKAFKFGKANSNVLRGAGAVVLYIDELKRYI 298
 DB 241 QSGRGADIMYGTVCWKRIEFDGKAFKFGKANSNVLRGAGAVVLYIDELKRYI 298
 RESULT 2
 AAM39641 ID AAM39641 standard; Protein; 298 AA.
 XX
 AC AAM39641;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 2786.
 XX
 KW Human; nootropic; immunosuppressant; cyostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US34263.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Ihu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI: 2001-442253/47.
 DR N-PSDB: AAI58797.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 PS Example 4; SEQ ID NO 2786; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAM38642-AA42213) with nootropic,
 CC immunosuppressant and cyostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Activin/Inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 CC
 XX
 SQ Sequence 298 AA;
 Query Match 100.0%; Score 1543; DB 22; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4, 6e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTEQAIISPAKDFLAGGIAAIAISKTAAPIERVKLLQVOHASKQIADKQKGIYDCIYR 60
 DB 1 MTEQAIISPAKDFLAGGIAAIAISKTAAPIERVKLLQVOHASKQIADKQKGIYDCIYR 60
 QY 61 IPEQGVLSFWKGNLANVIRYPTQALNFAFKDKYQKIFLGVDKHTQFWRYFAGNLAGS 120
 DB 61 IPEQGVLSFWKGNLANVIRYPTQALNFAFKDKYQKIFLGVDKHTQFWRYFAGNLAGS 120
 QY 121 GAAGATSLCFVYPLDPAFRTRLADVGKSGTEREFGDGLVYKITSDDGIRGLYQGFVS 180
 DB 121 GAAGATSLCFVYPLDPAFRTRLADVGKSGTEREFGDGLVYKITSDDGIRGLYQGFVS 180
 QY 181 VGGIITIRAAFGVYDTAKGMLPDPKNTHTIVSWMTAQTVTAAGVSYPPDTRRRMM 240
 DB 181 VGGIITIRAAFGVYDTAKGMLPDPKNTHTIVSWMTAQTVTAAGVSYPPDTRRRMM 240

```

OY 241 QSGRGADIMTGTVDCKRKIFRDEGKAFKFGAMSNVLRGGAFAVLVYDELKVI 298
DB 241 QSGRGADIMTGTVDCKRKIFRDEGKAFKFGAMSNVLRGGAFAVLVYDELKVI 298

RESULT 3
AAU01200
ID AAU01200 standard; Protein; 298 AA.
XX
AC AAU01200;
XX
DE 07-SEP-2001 (first entry)
XX
DE Human adenine nucleotide translocator-3 (ANT-3) protein.
XX
KW Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;
KW mitochondrial permeability transition pore component; cell survival;
KW mitochondrial core component; mitochondrial related disorder; cancer;
KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
XX
OS Homo sapiens.
XX
PN MO200132876-A2.
XX
PD 10-MAY-2001.
XX
PF 03-NOV-2000; 2000WO-US30535.
XX
PR 03-NOV-1999; 99US-0434354.
XX
PA (MITO-) MITOKOR.
XX
PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri IG;
PI Vejicelcebi G, Davis RE;
PI MPI: 2001-291054/30.
XX
DR N-PSDB; AAS05903.
XX
PT New nucleic acid expression constructs, useful for screening for agents
PT that alter mitochondrial permeability transition (MPT), comprises
PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
PT fused to energy transfer molecule -
XX
PS Disclosure; Fig 2; 186pp; English.
XX
CC The present sequence represents human adenine nucleotide translocator-3
CC (ANT-3) protein. ANT proteins are mitochondrial permeability
CC transition (MPT) pore components responsible for mediating transport
CC of ADP across the mitochondrial inner membrane. ANT proteins interact
CC with other mitochondrial core components e.g. cyclophilins to
CC regulate MPT. The present invention relates to a novel nucleic acid
CC expression construct comprising a promoter operably linked to a
CC polynucleotide encoding a mitochondrial pore component polypeptide
CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
CC expression construct can alter mitochondrial membrane permeability
CC transition and/or alter the interaction between mitochondrial core
CC components. The methods are useful for screening for agents that alter
CC MPT and/or cell survival. These agents are useful for the prevention or
CC treatment of diseases associated with altered mitochondrial function or
CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
CC mitochondrial encephalopathy, lactic acidosis, stroke,
CC hyperproliferative disorders e.g. cancer, and deafness.
XX
SQ Sequence 298 AA;
XX
Query Match 100.0%; Score 1543; DB 22; Length 298;
Best Local Similarity 100.0%; Pred. No. 4,66-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MTEQAISFAKDFLAGIAAIAISKTAVPIERVKLLLOVHASKQIAADKQYGIYDCIVR 60
|||||

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DB 1 MTEQAISFAKDFLAGIAAIAISKTAVPIERVKLLLOVHASKQIAADKQYGIYDCIVR 60
OY 61 IPKEGVLSFWMGNLAVNRYEPTQALNFAFDKXKQJFLGVDVDRHTQFWRFYAGNLASG 120
DB 61 IPKEGVLSFWMGNLAVNRYEPTQALNFAFDKXKQJFLGVDVDRHTQFWRFYAGNLASG 120
OY 121 GAAGATSLCEVYPLDFARTRLADYVKGSGTEERFRLGDCLVYKTRSDGIRGLYOGFSYS 180
DB 121 GAAGATSLCEVYPLDFARTRLADYVKGSGTEERFRLGDCLVYKTRSDGIRGLYOGFSYS 180
OY 181 VGGIIIRAAVYGVYDTAKGMLPDPKNTIHVSMIAQVTYVAVGVSYPTVRRRMM 240
DB 181 VGGIIIRAAVYGVYDTAKGMLPDPKNTIHVSMIAQVTYVAVGVSYPTVRRRMM 240
OY 241 QSGRGADIMTGTVDCKRKIFRDEGKAFKFGAMSNVLRGGAFAVLVYDELKVI 298
DB 241 QSGRGADIMTGTVDCKRKIFRDEGKAFKFGAMSNVLRGGAFAVLVYDELKVI 298

RESULT 4
AAU10380
ID AAU10380 standard; Protein; 298 AA.
XX
AC AAU10380;
XX
DE 14-FEB-2002 (first entry)
XX
DE Human adenine nucleotide translocator 3 (ANT3).
XX
KW Human; adenine nucleotide translocator; ANT;
KW mitochondrial matrix protein.
XX
OS Homo sapiens.
XX
PN WO200105944-A2.
XX
PD 15-NOV-2001.
XX
PF 11-MAY-2001; 2001WO-US15416.
XX
PR 11-MAY-2000; 2000US-0569327.
XX
PA (MITO-) MITOKOR.
XX
PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
PI Ghosh SS, Moos WH, Pel Y, Carroll AK;
PI MPI: 2002-055598/07.
XX
DR N-PSDB; AAS16690.
XX
PT Novel recombinant expression construct for producing adenine nucleotide
PT translocator polypeptides, comprises a regulated promoter linked to
PT nucleic acid encoding the polypeptide -
XX
PS Example 3; Fig 2; 147pp; English.
XX
CC The invention relates to a recombinant expression construct (I)
CC comprising a regulated promoter operably linked to a nucleic acid
CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
CC proteins mediate the exchange of ATP synthesized in the mitochondrial
CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
CC culturing the host cell. (I) is also useful for targeting a polypeptide
CC of interest to a mitochondrial membrane, where ANT polypeptide is
CC expressed as a fusion protein with the polypeptide of interest.
CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
CC useful for identifying an agent that binds to an ANT polypeptide. ANT
CC ligand is useful for determining the presence of an ANT polypeptide,
CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
CC ANT from a biological sample, where the ANT ligand is covalently or non-
CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
CC useful for identifying an agent that interacts with an ANT polypeptide.
CC The present sequence represents the amino acid sequence of human ANT3.

```

XX Sequence 298 AA;

Query Match 100.0%; Score 1543; DB 23; Length 298;
Best Local Similarity 100.0%; Pred. No. 4, 6e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQAIISFAKDFLAGGIAAISKTAAPIERVKLLQVQASKQIADKQYKGIQDICTV 60
DB 1 MTEQAIISFAKDFLAGGIAAISKTAAPIERVKLLQVQASKQIADKQYKGIQDICTV 60
QY 61 IPKEQGLSFWKRNLANVIRYFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 120
DB 61 IPKEQGLSFWKRNLANVIRYFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 120
QY 121 GAAGATSLCFVYPLDFARTRLADVKSCTEREPRGIGDCLVITKSDGIRGLYQGSVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADVKSCTEREPRGIGDCLVITKSDGIRGLYQGSVS 180
QY 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTHTVSMIAQVTAAGVVSYPEDTVRRRMM 240
DB 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTHTVSMIAQVTAAGVVSYPEDTVRRRMM 240
QY 241 QSGRKADIMYTGTVDCWKRIFFRDEGKAFKFGAMSVNLKMGAFVLVLYDELKVI 298
DB 241 QSGRKADIMYTGTVDCWKRIFFRDEGKAFKFGAMSVNLKMGAFVLVLYDELKVI 298

RESULT 5
ID AAM41427 standard; Protein: 323 AA.
AC AAM41427;
XX 22-OCT-2001 (first entry)
DT Human polypeptide SEQ ID NO 6358.
DE Human polypeptide SEQ ID NO 6358.
XX Human; neurotrophic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW Leukaemia.
XX Homo sapiens.
OS
XX MO200153312-A1.
PN
XX 26-JUL-2001.
PD
XX 26-DEC-2000; 2000MO-US34263.
PF
XX 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
DR N-PSDB; AAI60583.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -

XX Example 2: SEQ ID NO 6358; 10078pp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and
PS the encoded polypeptides (AAM38642-AAM42213) with neurotrophic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC activation/inhibition of the activities such as: immune system suppression,
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX

QY 1 MTEQAIISFAKDFLAGGIAAISKTAAPIERVKLLQVQASKQIADKQYKGIQDICTV 60
DB 26 MTEQAIISFAKDFLAGGIAAISKTAAPIERVKLLQVQASKQIADKQYKGIQDICTV 85
QY 61 IPKEQGLSFWKRNLANVIRYFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 120
DB 61 IPKEQGLSFWKRNLANVIRYFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 120
QY 121 GAAGATSLCFVYPLDFARTRLADVKSCTEREPRGIGDCLVITKSDGIRGLYQGSVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADVKSCTEREPRGIGDCLVITKSDGIRGLYQGSVS 180
QY 146 GAAGATSLCFVYPLDFARTRLADVKSCTEREPRGIGDCLVITKSDGIRGLYQGSVS 205
DB 146 GAAGATSLCFVYPLDFARTRLADVKSCTEREPRGIGDCLVITKSDGIRGLYQGSVS 205
QY 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTHTVSMIAQVTAAGVVSYPEDTVRRRMM 240
DB 206 VGGIIIRAAVFGVYDTAKGMLPDPKNTHTVSMIAQVTAAGVVSYPEDTVRRRMM 265
QY 241 QSGRKADIMYTGTVDCWKRIFFRDEGKAFKFGAMSVNLKMGAFVLVLYDELKVI 298
DB 266 QSGRKADIMYTGTVDCWKRIFFRDEGKAFKFGAMSVNLKMGAFVLVLYDELKVI 323

RESULT 6
ID AAO18516 standard; Protein: 298 AA.
AC AAO18516;
XX 11-OCT-2002 (first entry)
DT Human insulin receptor signaling modifier SEQ ID NO: 54.
DE Human insulin receptor signaling modifier
XX Human; insulin receptor signaling; insulin receptor signaling modifier;
KW IEM; diabetes; metabolic syndrome; antidiabetic.
XX
XX Homo sapiens.
OS
XX MO200255664-A2.
PN
XX 18-JUL-2002.
PD
XX 11-JAN-2002; 2002MO-US01048.
PF
XX 12-JAN-2001; 2001US-261226P.
PR 12-JAN-2001; 2001US-261303P.
PR 12-JAN-2001; 2001US-261304P.
PR 12-JAN-2001; 2001US-261335P.
PR 12-JAN-2001; 2001US-261336P.

Db 61 IPKEQEVLSFWRGNLANVIRYFPFOALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADVKGSGTEREFGDGLVYITKSDGIRGLYOGFSVS 180
 Db 121 GAAGATSLCFVYPLDFARTRLADVKGAGEREFRGLDGLVYITKSDGIRGLYOGFSVS 180
 QY 181 VGGIIIRAAVFGVYDPAKGMPLDPKNTHTIVSMMIAQVTAVAGVSYFPDVRRRMM 240
 Db 181 VGGIIIRAAVFGVYDPAKGMPLDPKNTHTIVSMMIAQVTAVAGVSYFPDVRRRMM 240
 QY 241 QSGRKADIMYTGTVDCWKRIFRDEGKAFKFGKAMSIVLRGNGAFVLYLYDELK 296
 Db 241 QSGRKADIMYTGTVDCWKRIFRDEGKAFKFGKAMSIVLRGNGAFVLYLYDELK 296
 RESULT 8
 AAU01199
 ID AAU01199 standard; Protein; 298 AA.
 AC AAU01199;
 XX 07-SEP-2001 (first entry)
 DE Human adenine nucleotide translocator-2 (ANT-2) protein.
 XX
 KW Human; adenine nucleotide translocator-2; ANT-2; MPT; cyclophilin;
 KM mitochondrial permeability transition pore component; cell survival;
 KM mitochondrial core component; mitochondrial related disorder; cancer;
 KM Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200132876-A2.
 PD 10-MAY-2001.
 PF 03-NOV-2000; 2000WO-US30535.
 PR 03-NOV-1999; 99US-0434354.
 PA (MITO-) MITOKOR.
 PI Murphy AN, Cleverger W, Wiley SE, Andreyev AV, Frigert LG;
 PI Velicelebi G, Davis RE;
 DR MPI; 2001-291054/30.
 XX N-PSDB; AAS05902.
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 PS Disclosure; Fig 2; 186pp; English.
 CC The present sequence represents human adenine nucleotide translocator-2
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,

CC hyperproliferative disorders e.g. cancer, and deafness.
 XX
 SQ Sequence 298 AA;
 Query Match 94.2%; Score 1454; DB 22; Length 298;
 Best Local Similarity 92.6%; Pred. No. 1.7e-147;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTEQALISFANDFLAGIAAISTKAVAPIRRVKLLLOVHASKQIADKQKGIYDCIVR 60
 Db 1 MTEQALISFANDFLAGIAAISTKAVAPIRRVKLLLOVHASKQIADKQKGIYDCIVR 60
 QY 61 IPKEQEVLSFWRGNLANVIRYFPFOALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
 Db 61 IPKEQEVLSFWRGNLANVIRYFPFOALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADVKGSGTEREFGDGLVYITKSDGIRGLYOGFSVS 180
 Db 121 GAAGATSLCFVYPLDFARTRLADVKGAGEREFRGLDGLVYITKSDGIRGLYOGFSVS 180
 QY 181 VGGIIIRAAVFGVYDPAKGMPLDPKNTHTIVSMMIAQVTAVAGVSYFPDVRRRMM 240
 Db 181 VGGIIIRAAVFGVYDPAKGMPLDPKNTHTIVSMMIAQVTAVAGVSYFPDVRRRMM 240
 QY 241 QSGRKADIMYTGTVDCWKRIFRDEGKAFKFGKAMSIVLRGNGAFVLYLYDELK 296
 Db 241 QSGRKADIMYTGTVDCWKRIFRDEGKAFKFGKAMSIVLRGNGAFVLYLYDELK 296
 RESULT 9
 AAU10379
 ID AAU10379 standard; Protein; 298 AA.
 AC AAU10379;
 XX 14-FEB-2002 (first entry)
 DE Human adenine nucleotide translocator 2 (ANT2).
 XX
 KW Human; adenine nucleotide translocator; ANT; ss;
 KM mitochondrial matrix protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200185944-A2.
 PD 15-NOV-2001.
 PF 11-MAY-2001; 2001WO-US15416.
 PR 11-MAY-2000; 2000US-0569327.
 PA (MITO-) MITOKOR.
 PI Anderson CM, Davis RE, Cleverger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS, Moos WH, Pei Y, Carroll AK;
 DR MPI; 2002-055598/07.
 XX N-PSDB; AAS16689.
 PT Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide -
 XX
 PS Claim 44; Fig 2; 147pp; English.
 CC The invention relates to a recombinant expression construct (I)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (I) is also useful for targeting a polypeptide

CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide.
 CC preferably AN1, AN2 or AN3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human AN2.
 CC
 XX
 SO Sequence 298 AA:

Query Match 94.2%; Score 1454; DB 23; Length 298;
 Best Local Similarity 92.6%; Pred. No. 1.7e-147;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQAIISFAKDFLAGIAAISKTAAPIERVKLLQVGHASKQIAADKQYGYDVCYR 60
 DB 1 MTDAAISFAKDFLAGVAAISKTAAPIERVKLLQVGHASKQITADKQYGYDVCYR 60
 QY 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFDKXKQIPLGVDKHTQFWRFAGNLASG 120
 DB 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFDKXKQIPLGVDKHTQFWRFAGNLASG 120
 QY 121 IPKEGVLSFMRGNLANVIRYPTQALNFAFDKXKQIPLGVDKHTQFWRFAGNLASG 180
 DB 121 IPKEGVLSFMRGNLANVIRYPTQALNFAFDKXKQIPLGVDKHTQFWRFAGNLASG 180
 QY 121 GAAGATSLCFEYVPLDFARTRLAADVKGSGTEREFRGLDCLVKITKSDIRGLYOGFSYS 180
 DB 121 GAAGATSLCFEYVPLDFARTRLAADVKGSGTEREFRGLDCLVKITKSDIRGLYOGFSYS 180
 QY 181 VOGIIIRAAAYFGVYDTAKGMLPDPKNTHTIVVSMIAQTVAVAGVSTPFTVRRMM 240
 DB 181 VOGIIIRAAAYFGVYDTAKGMLPDPKNTHTIVVSMIAQTVAVAGVSTPFTVRRMM 240
 QY 241 OSGRKADIMYTGTVDCRKIFRDEGKAFKFGANSNVLRGGAFLVLYDELK 296
 DB 241 OSGRKADIMYTGTVDCRKIFRDEGKAFKFGANSNVLRGGAFLVLYDELK 296

RESULT 10
 ABR41715
 ID ABR41715 standard; Protein: 429 AA.
 XX
 AC ABR41715;
 XX
 DT 02-JUN-2003 (first entry)
 XX
 DE Human DITHP organelle-associated protein.
 XX
 KM Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
 KM cancer; cell proliferative disorder; autoimmune disorder;
 KM inflammatory disorder; infection; hormonal disorder; metabolic disorder;
 KM neurological disorder; gastrointestinal disorder; transport disorder;
 KM connective tissue disorder; drug screening; proteome analysis;
 KM gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
 KM disease model; toxicological testing; transcript imaging;
 KM organelle-associated protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200297031-A2.
 XX
 PD 05-DEC-2002.
 PF 27-MAR-2002; 2002MO-US10056.
 XX
 PR 28-MAR-2001; 2001US-279619P.
 PR 29-MAR-2001; 2001US-280067P.
 PR 29-MAR-2001; 2001US-280068P.
 PR 16-MAY-2001; 2001US-291280P.
 PR 17-MAY-2001; 2001US-291829P.
 PR 17-MAY-2001; 2001US-291849P.
 PR 19-JUN-2001; 2001US-299428P.
 PR 20-JUN-2001; 2001US-299776P.

PR 20-JUN-2001; 2001US-300001P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshay SR;
 PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleeferd Y, Gerstin EH;
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 PI Flores V, Marwaha R, Lo A, Lan RX, Urashka ME;
 XX
 DR MPI: 2003-129518/12.
 DR N-PSDB; ACC46652.
 XX
 PT Novel human diagnostic and therapeutic polypeptide useful for
 PT identifying test compound which specifically binds to a polypeptide
 PT encoded by human diagnostic and therapeutic polynucleotide, and to
 PT induce antibodies
 XX
 PS Claim 27; SEQ ID NO 1250; 591bp; English.
 XX

The invention relates to novel human diagnostic and therapeutic
 CC polynucleotides designated dithp (ACC46080-ACC46749) and to their
 CC encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates
 CC to polynucleotide sequences at least 90% identical to the dithp cDNA
 CC sequences of the invention; recombinant vectors, host cells and
 CC transgenic organisms comprising a dithp nucleic acid sequence; the
 CC recombinant production of DITHP proteins; antibodies specific for DITHP
 CC proteins; microarrays comprising dithp nucleic acid sequences; methods
 CC of detecting dithp nucleotide and protein sequences; methods of screening
 CC for compounds which specifically bind a DITHP protein; and methods of
 CC assessing the toxicity of test compounds using a dithp hybridisation
 CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
 CC diagnosis of a wide variety of conditions including cancer and other cell
 CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
 CC viral, fungal or parasitic infections; hormonal disorders; metabolic
 CC disorders; neurological disorders; gastrointestinal disorders; transport
 CC disorders; and connective tissue disorders. They may also be used to
 CC screen for modulators of protein activity or gene expression. DITHP
 CC proteins can additionally be used in analysis of the proteome of a tissue
 CC or cell type and to induce antibodies. The dithp nucleic acids are
 CC additionally useful in somatic or germline gene therapy of the disorders
 CC mentioned above, as a source of antisense sequences, as a source of
 CC probes and primers, in genotyping and identification of individuals, in
 CC the generation of transgenic animal models of human disease or knock in
 CC humanised animals, in toxicological testing, and in transcript imaging.
 CC The present sequence represents a DITHP protein which is an organelle-
 CC associated protein.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX

SO Sequence 429 AA:

Query Match 91.9%; Score 1418; DB 24; Length 429;
 Best Local Similarity 95.2%; Pred. No. 2e-143;
 Matches 277; Conservative 3; Mismatches 5; Indels 6; Gaps 2;

QY 1 MTEQAIISFAKDFLAGIAAISKTAAPIERVKLLQVGHASKQIAADKQYGYDVCYR 60
 DB 26 MTEQAIISFAKDFLAGIAAISKTAAPIERVKLLQVGHASKQIAADKQYGYDVCYR 85
 QY 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFDKXKQIPLGVDKHTQFWRFAGNLASG 120
 DB 86 IPKEGVLSFMRGNLANVIRYPTQALNFAFDKXKQIPLGVDKHTQFWRFAGNLASG 145
 QY 121 GAAGATSLCFEYVPLDFARTRLAADVKGSGTEREFRGLDCLVKITKSDIRGLYOGFSYS 180
 DB 146 GAAGATSLCFEYVPLDFARTRLAADVKGSGTEREFRGLDCLVKITKSDIRGLYOGFSYS 205
 QY 181 VOGIIIRAAAYFGVYDTAKGMLPDPKNTHTIVVSMIAQTVAVAGVSTPFTVRRMM 240
 DB 206 VOGIIIRAAAYFGVYDTAKGMLPDPKNTHTIVVSMIAQTVAVAGVSTPFTVRRMM 265

QY 241 QSGRRGADIMYTGTVDCMRKIFRDEGGAFFKGA-W-----SNVLRGMGA 285
 Db 266 QSGRRGADIMYTGTVDCMRKIFRDEGGAFFKGSMMQATLADLESPPSA 316

RESULT 11

AA661169 standard; Protein: 298 AA.

AA661169;

28-SEP-1998 (first entry)

Ant1 protein.

Ant1; Adenine nucleotide translocator; cloning; screening;
 DNA Tag dideoxy terminator cycle sequencing; oxidative phosphorylation;
 probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;
 hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;
 lactic acidosis; degenerative muscle disease.

Mus sp.

MO9819714-A1.

14-MAY-1998.

31-OCT-1997; 97MO-US19882.

01-NOV-1996; 96US-0030017.

(UYEM-) UNIV EMORY.

Graham BC, Macgregor GR, Wallace DC;

WPI; 1998-286608/25.

N-PDB; AAV36479.

Mice lacking heart-muscle adenine nucleotide translocator protein -
 useful as model for mitochondrial myopathy and hypertrophic
 cardiomyopathy in animals and to test therapeutic compositions or
 gene therapies

Disclosure; Page 39-40; 61pp; English.

The present sequence is the mouse Ant1 protein, the cDNA producing this
 polypeptide is cloned by screening a mouse heart cDNA library with the
 human Ant1 cDNA as a probe. The Ant1 cDNA sequence was determined by DNA
 Tag dideoxy terminator cycle sequencing. The Ant1 protein is encoded by
 CC the Ant1 locus, a nuclear gene on chromosome 8. This protein is required
 CC in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP
 CC which can then be converted into ATP. An Ant1 homozygous mutant would
 CC thus be defective in OXPHOS which results in disease in oxidative
 CC metabolism dependent tissues. This mouse Ant1 homozygous mutant can be
 CC used as a model system for fascioscapular humeral muscular dystrophy,
 CC hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model
 CC systems can be used to test possible therapeutic compounds which
 CC increase/decrease ATP and ADP exchange across the mitochondrial membrane
 CC independent of Ant1.

Sequence 298 AA;

Query Match 91.5%; Score 1412; DB 19; Length 298;
 Best Local Similarity 88.6%; Pred. No. 5.4e-143;
 Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 MNEQALSFAPKDFLAGGTAIAISTAVAPIERVKLLLOVQHASKQIADKQYKIVTCYR 60

Db 1 MGOQALSPKDFLAGGTAIAAVSTAVAPIERVKLLLOVQHASKQISAEKQYKGIIDCVYR 60

QY 61 IRKQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120
 Db 61 IRKQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120

QY 121 GAAGATSLCYVYPLDFARTLADVGKSGTEREFGIGDCLVITKSDGIRGLYQGSVS 180
 Db 121 GAAGATSLCYVYPLDFARTLADVGKSSQREFNGIGDCLTKIFKSDGLKGLYQGSVS 180

QY 181 VOGIIYRAVYFGVYDPAKGLPDKRTHIVSMINQYTNAYAGVSYFEDVRRMM 240

Db 181 VOGIIYRAVYFGVYDPAKGLPDKRTHIVSMINQYTNAYAGVSYFEDVRRMM 240

QY 241 QSGRRGADIMYTGTVDCMRKIFRDEGGAFFKGAWSNVLRGMGAFLVLYDELKRYI 298

Db 241 QSGRRGADIMYTGTVDCMRKIANDEGANAFKGAWSNVLRGMGAFLVLYDELKRYI 298

RESULT 12

ABU53219 standard; Protein: 293 AA.

ABU53219;

14-APR-2003 (first entry)

Human metabolism-associated DKFzphes3_35n12 homologue #1.

Human; gene therapy; vaccine; disease treatment; detection.

Homo sapiens.

WO200112659-A2.

22-FEB-2001.

18-AUG-2000; 2000MO-IB01496.

18-AUG-1999; 99US-0149499.

28-SEP-1999; 99US-0156503.

(GEHU-) GERMAN HUMAN GENOME PROJECT.

Wiemann S;

WPI; 2001-327840/34.

Nucleic acids having the sequences of clones isolated from libraries of
 different human tissues, useful in recombinant DNA methodologies -
 Example III; Page 850; 1095pp; English.

This invention describes novel polynucleotides and polypeptides isolated
 from human cDNA libraries which can be used for gene therapy or in
 vaccines. The polynucleotides of the invention and antibodies encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. The products of the
 CC invention may also be used to identify modulators of expression and
 CC activity and to down regulate expression and activity. The antibodies of
 CC the invention may also be used as diagnostic agents for detecting the
 CC presence of polypeptides in samples. This sequence represents a homologue
 CC of a polypeptide described in the disclosure of the invention.

Sequence 293 AA;

Query Match 91.1%; Score 1406; DB 22; Length 293;
 Best Local Similarity 90.1%; Pred. No. 2.3e-142;
 Matches 263; Conservative 17; Mismatches 12; Indels 0; Gaps 0;

QY 5 AIFAPKDFLAGGTAIAISTAVAPIERVKLLLOVQHASKQIADKQYKIVTCYR 64

Db 1 AIFAPKDFLAGGTAIAAVSTAVAPIERVKLLLOVQHASKQISAEKQYKGIIDCVYR 60

QY 65 OGVLSPWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 124
 Db 61 OGVLSPWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120

QY 125 ATSLCFVYPLDFAFTRRLADYVKGSGTEREFGGLDCLVKTIRKSDGIRGLYOGFSVSGCI 184
 DB 121 ATSLCFVYPLDFAFTRRLADYVKGSGTEREFGGLDCLVKTIRKSDGIRGLYOGFSVSGCI 180
 QY 185 IITRAAYGVYDTAKGMLPDPKNTHTIVSMMIAQVTVAVAGVSYPTPTVRRMMQSGR 244
 DB 181 IITRAAYGVYDTAKGMLPDPKNTHTIVSMMIAQSVTVAVAGVSYPTPTVRRMMQSGR 240
 QY 245 KGADIMYGTGTCWKRIFRDEGKAFKFGAMSNTVRGKGAFVLYLDELKK 296
 DB 241 KGADIMYGTGTCWKRIFRDEGKAFKFGAMSNTVRGKGAFVLYLDELKK 292
 RESULT 13
 AAY71031
 ID AAY71031 standard; Protein: 297 AA.
 AC AAY71031;
 DT 29-AUG-2000 (first entry)
 DE Human adenine nucleotide translocator AMT1.
 XX Human; adenine nucleotide translocator; AMT1; mitochondria; ADP; ATP;
 KM adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KM mitochondrial permeability transition; neuroprotective; nootropic;
 KM antiParkinsonian; cytoskeletal; antidiabetic; anticonvulsant; neuroleptic;
 KM antisporitic; cerebroprotective; therapeutic; screening; poriasis;
 KM Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KM diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KM mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
 KM mitochondrial diabetes and deafness; hyperproliferative disorder;
 KM myoclonic epilepsy red ragged fibre syndrome.
 XX Homo sapiens.
 OS
 PN WO200026370-A2.
 PD 11-MAY-2000.
 PE 03-NOV-1999; 99WO-US25883.
 PF 03-NOV-1998; 98US-0185904.
 PR 08-SEP-1999; 99US-0393441.
 XX (MITO-) MITOKOR.
 PA
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 DR MPI: 2000-365619/31.
 DR N-PSDB: AAD00519.
 XX Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 PS Claim 44; Page 172; 175pp; English.

CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator AMT1 from human brain.
 XX
 SQ Sequence 297 AA:
 Query Match 89.8%; Score 1385.5; DB 21; Length 297;
 Best Local Similarity 87.2%; Pred. No. 3.8e-140;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
 QY 1 MTEQALISFKADPLAGIAAISKTAAPIERVKLLQVOHASKQIADKQYGIYDCIVR 60
 DB 1 MGDHAWSPFLDKPAGVAVAASVKTAPPIERVKLLQVOHASKQISAEKQYGIIDCVVR 60
 QY 61 IPKEGVLSFWRGNLANVRYRPTQALNFAFDKXKQITLGGVDKHTQWRFAFNLSG 120
 DB 61 IPKEGVLSFWRGNLANVRYRPTQALNFAFDKXKQITLGGVDKHTQWRFAFNLSG 120
 QY 121 GAAGATSLCFVYPLDFAFTRRLADYVKGSGTEREFGGLDCLVKTIRKSDGIRGLYOGFSVS 180
 DB 121 GAAGATSLCFVYPLDFAFTRRLADYVKGSGTEREFGGLDCLVKTIRKSDGIRGLYOGFSVS 179
 QY 181 VOGIITTRAAAYGVYDTAKGMLPDPKNTHTIVSMMIAQVTVAVAGVSYPTPTVRRMMQ 240
 DB 181 VOGIITTRAAAYGVYDTAKGMLPDPKNTHTIVSMMIAQSVTVAVAGVSYPTPTVRRMMQ 239
 QY 241 OSGRKGADIMYGTGTCWKRIFRDEGKAFKFGAMSNTVRGKGAFVLYLDELKKYI 298
 DB 241 OSGRKGADIMYGTGTCWKRIFRDEGKAFKFGAMSNTVRGKGAFVLYLDELKKYI 297
 RESULT 14
 AAD01198
 ID AAD01198 standard; Protein: 297 AA.
 AC AAD01198;
 DT 07-SEP-2001 (first entry)
 DE Human adenine nucleotide translocator-1 (ANT-1) protein.
 XX Human; adenine nucleotide translocator-1; ANT-1; MPT; cyclophilin;
 KM mitochondrial permeability transition pore component; cell survival;
 KM mitochondrial core component; mitochondrial related disorder; cancer;
 KM Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX Homo sapiens.
 OS
 PN WO200132876-A2.
 PD 10-MAY-2001.
 PE 03-NOV-2000; 2000WO-US30535.
 PR 03-NOV-1999; 99US-0434354.
 XX (MITO-) MITOKOR.
 PA
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Fritgerl IG;
 PI Velicelebi G, Davis RE;
 DR MPI: 2001-291054/30.
 DR N-PSDB: AAS05901.
 XX New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 PS Disclosure; Fig 2; 186pp; English.
 CC The present sequence represents human adenine nucleotide translocator-1
 CC (ANT-1) protein. ANT proteins are mitochondrial permeability

COMPUTER: IBM PC compatible

ORGANISM: Homo sapien

US-09-434-354-47

Query Match	89.8%;	Score 1385.5;	DB 4;	Length 297;
Best Local Similarity	-87.2%;	Pred. NO. 2.9e-148;		
Matches 260; Conservative	21;	Mismatches 16;	Indels 1;	Gaps 1

[illegible]

RESULT 5
US-09-996-243-289

Sequence 289, Application US/09996243
; Patent No. 6478825

APPLICANT: Ashkonat

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary

APPLICANT: Godowski, Paul J

APPLICANT: Grimaldi, J. Chr

APPLICANT: Gurney, Austin L

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas

APPLICANT: Stewart, Timothy

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Collin

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

1. TITLE OF INVENTION: **Secret**

FILE OF INVENTION: ACIDS
FILE REFERENCE: P2730P1C13

CURRENT APPLICATION NUMBER:

; CURRENT FILING DATE: 2001-

PRIOR APPLICATION NUMBER: 6
PRIOR FILING DATE: 1997-06-

PRIOR APPLICATION NUMBER: 6

PRIOR FILING DATE: 1997-10-

PRIOR APPLICATION NUMBER: 6
PRIOR FILING DATE: 1987-11

PRIOR APPLICATION NUMBER: 6

;
PRIOR FILING DATE: 1997-11-

PRIOR APPLICATION NUMBER: 6
PRIOR FILING DATE: 1007-11

PRIOR FILING DATE: 1997-11-
; PRIOR APPLICATION NUMBER: 6

PRIOR FILING DATE: 1998-02-

PRIOR FILING DATE:	1998-03-20
PRIOR APPLICATION NUMBER:	60/083322
PRIOR FILING DATE:	1998-04-28
PRIOR APPLICATION NUMBER:	60/084600
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/087106
PRIOR FILING DATE:	1998-05-28
PRIOR APPLICATION NUMBER:	60/087607
PRIOR FILING DATE:	1998-06-02
PRIOR APPLICATION NUMBER:	60/087609
PRIOR FILING DATE:	1998-06-02
PRIOR APPLICATION NUMBER:	60/087755
PRIOR FILING DATE:	1998-06-02
PRIOR APPLICATION NUMBER:	60/087827
PRIOR FILING DATE:	1998-06-03
PRIOR APPLICATION NUMBER:	60/088021
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088028
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088030
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088033
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088167
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088202
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088555
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088742
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088810
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088822
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088822
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088856
PRIOR FILING DATE:	1998-06-11
PRIOR APPLICATION NUMBER:	60/088873
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/089512
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/089513
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089596

1	PRIOR FILING DATE:	1998-06-17
2	PRIOR APPLICATION NUMBER:	60/089592
3	PRIOR FILING DATE:	1998-06-17
4	PRIOR APPLICATION NUMBER:	60/089600
5	PRIOR FILING DATE:	1998-06-17
6	PRIOR APPLICATION NUMBER:	60/089633
7	PRIOR FILING DATE:	1998-06-17
8	PRIOR APPLICATION NUMBER:	60/089801
9	PRIOR FILING DATE:	1998-06-17
10	PRIOR APPLICATION NUMBER:	60/089907
11	PRIOR FILING DATE:	1998-06-19
12	PRIOR APPLICATION NUMBER:	60/089923
13	PRIOR FILING DATE:	1998-06-19
14	PRIOR APPLICATION NUMBER:	60/090246
15	PRIOR FILING DATE:	1998-06-22
16	PRIOR APPLICATION NUMBER:	60/090255
17	PRIOR FILING DATE:	1998-06-22
18	PRIOR APPLICATION NUMBER:	60/090256
19	PRIOR FILING DATE:	1998-06-22
20	PRIOR APPLICATION NUMBER:	60/090349
21	PRIOR FILING DATE:	1998-06-23
22	PRIOR APPLICATION NUMBER:	60/090355
23	PRIOR FILING DATE:	1998-06-23
24	PRIOR APPLICATION NUMBER:	60/090429
25	PRIOR FILING DATE:	1998-06-24
26	PRIOR APPLICATION NUMBER:	60/090431
27	PRIOR FILING DATE:	1998-06-24
28	PRIOR APPLICATION NUMBER:	60/090435
29	PRIOR FILING DATE:	1998-06-24
30	PRIOR APPLICATION NUMBER:	60/090444
31	PRIOR FILING DATE:	1998-06-24
32	PRIOR APPLICATION NUMBER:	60/090445
33	PRIOR FILING DATE:	1998-06-24
34	PRIOR APPLICATION NUMBER:	60/090557
35	PRIOR FILING DATE:	1998-06-24
36	PRIOR APPLICATION NUMBER:	60/090567
37	PRIOR FILING DATE:	1998-06-24
38	PRIOR APPLICATION NUMBER:	60/090544
39	PRIOR FILING DATE:	1998-06-24
40	PRIOR APPLICATION NUMBER:	60/090542
41	PRIOR FILING DATE:	1998-06-24
42	PRIOR APPLICATION NUMBER:	60/090630
43	PRIOR FILING DATE:	1998-06-25
44	PRIOR APPLICATION NUMBER:	60/090687
45	PRIOR FILING DATE:	1998-06-25
46	PRIOR APPLICATION NUMBER:	60/090694
47	PRIOR FILING DATE:	1998-06-25
48	PRIOR APPLICATION NUMBER:	60/090655
49	PRIOR FILING DATE:	1998-06-25
50	PRIOR APPLICATION NUMBER:	60/090666
51	PRIOR FILING DATE:	1998-06-25
52	PRIOR APPLICATION NUMBER:	60/090822
53	PRIOR FILING DATE:	1998-06-26
54	PRIOR APPLICATION NUMBER:	60/090853
55	PRIOR FILING DATE:	1998-06-26
56	PRIOR APPLICATION NUMBER:	60/091360
57	PRIOR FILING DATE:	1998-07-01
58	PRIOR APPLICATION NUMBER:	60/091478
59	PRIOR FILING DATE:	1998-07-02
60	PRIOR APPLICATION NUMBER:	60/091544
61	PRIOR FILING DATE:	1998-07-01
62	PRIOR APPLICATION NUMBER:	60/091519
63	PRIOR FILING DATE:	1998-07-02

1 PRIOR APPLICATION NUMBER: 60/091656
 2 PRIOR FILING DATE: 1998-07-02
 3 PRIOR APPLICATION NUMBER: 60/091633
 4 PRIOR FILING DATE: 1998-07-02
 5 PRIOR APPLICATION NUMBER: 60/091978
 6 PRIOR FILING DATE: 1998-07-07
 7 PRIOR APPLICATION NUMBER: 60/091982
 8 PRIOR FILING DATE: 1998-07-07
 9 PRIOR APPLICATION NUMBER: 60/092182
 10 PRIOR FILING DATE: 1998-07-09

Query Match	20.3%;	Score 314;	DB 4;	Length 469;
Best Local Similarity	30.1%;	Pred. No. 7.8e-27;		
Matches	89;	Conservative	60;	Mismatches 115;
			Indels	32;
			Gaps	11;

```

OY 10 KDFLAGGAAIASTKVAIVPIERVKLLTLOYHASKIOADKOYKQAYDCLVRIPEKQVYS 69
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 188 RHLVAGGAGAVSRICSTAPDLRLKILMOY-HASR-----SNNKGIYGGTOMIREGCANS 241
OY 70 FWRGNLANVIRYFPTQALNFAFKDKYKQIETLIGVDKHTQFWRYFAGNLASGGAAGATSLC 129
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 242 LWRGNGIYNLKAIPESAIKFEAYEQIKR--LVGSDPET--LRHERLVAGSLAGIAAGS 296
OY 130 FYVPLDFAFTRILAAVQKSGCTERERGLDCLVYKTKSGINGIYOGFESVQGLIIYRA 189
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 297 STIPEVILKTRRA--LRKTG---QYSGIMDCARRILARBGVAALFYKGYVPMNIGIILPYAG 351
OY 190 AAFGVYDFAKGM-----LPDPNTHIIVSWSMILAOYTAIVAG--VVSYPFDVRRRMM 240
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 352 IDLAVYETLKNAMIOHYAVNSADPG---VFYILACGTSSPSCGGLASPLALVRRMQA 407
OY 241 OSGRGDALIMTYGTDCKRKITPRDEGGRKAFYFGANSNVLRGAGAV-LYVIDELK 295
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 408 QASIEGAEVWSSL--FKHILRTGAGFGLYGLAPNEFKKVLIPAVSISVYVENLK 461

```

```

RESULT 6
US-09-188-930-339
Sequence 339, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REFERENCE: 11000.1011c1
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 469
TYPE: PRT
ORGANISM: Mouse
US-09-188-930-339

```

	Query Match	20.2%	Score 311;	DB 3:	Length 469;
	Best Local Similarity	29.4%;	Pred. No. 1.7e-26;		
	Matches	88;	Conservative	62;	Mismatches 111; Indels 38; Gaps 11.
OY	10 KDLFAGIAAISTAVAPIERVKLLQVHASKOIALDKDYKGIIVDCIVRIPEEQGYLS	69	:	: :: :	::
Dd	188 RHLYVGAGGAGVASRTCTAPLDRLRVLMGV-HASR---- <td>241</td> <td>:</td> <td>: :: :</td> <td> :: </td>	241	:	: :: :	::
OY	70 FMRGNLANVIAYEFPOLNFAFKDXYKOIFLGSVDKHQTFMRYPAIGNLASGAAGAATSLC	129	:	: :: :	::
Dd	242 LMRNGINVLTKIAESAIKFMYAQMKR--LVGSDQE-----LRIRFLVAASSLAGATIQS	296	:	: :: :	::
OY	130 FYVDLPARTRLAADVCSTGEREFRGIDGLCVKITNSDGIRGLCYOGFSVSVOGITTYRA	189	:	: :: :	::

```

Db      297 SIYPPEVLTRMA--LRKGG--QYSGLDCARRLAEGVAAAYKXGIPNMGIIIPYAG 351
Oy      190 AFGGVYDAKAGLDPKRNTHI-----VYSMTLAQVTVAVAG-VYSPEPDYRRR 237
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      352 IDLAAYETL-----KRWLQRAYVANSADGVPFLACGIIISTCQGLASYPALAYRTR 404
Oy      238 MAMQSRKKAADIMTYGYDCKRKIRFDGSGKAFFEGAMSNVLRGMGAFV-LVIYDELK 295
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      405 MQAQASITCEAPAEVYMSLL--FQQLIRTEGACGLVRLGLNAPNKKYIAPVSIYVEYLK 461

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RESULT 7
US-09-312-283C-339
Sequence 339, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Ounust, Rene
APPLICANT: Marison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TYPE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011C
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 339
LENGTH: 469
TYPE: PR1
ORGANISM: Mouse
US-09-312-283C-339

```

Query Match	20.2%	Score 311	DB 4	Length 469
Best Local Similarity	29.4%	Pred. No.	1.7e-26	
Matches 88	Conservative 62	Mismatches 111	Indels 38	Gaps 11

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Oy      70  FMNGNLANYIRIFPTQALNFAFKDKYKQJOTLFGVDKHTQFMRYIRFAGNLASGAAGATSLC 122
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db      242  LMRGNININYLKTAPEBAIKFMAYEOMKR--LVGSDQET---LRHERVAVASLGALIAQOS 298
Oy      130  FVYPLDPAFRLAADVGKSTGEREPFGDCIVKPTKSDGIRGLYOGFVSVOGIIYRA 189
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db      297  STIPMEVUKTRMA--LRKTG---QYSGMLDCARRILAEVGAATFKGIIIPMLGIIPYAG 355
Oy      190  AYFGVYDTAKGMLPDKRNTHI-----VSSWMLAQVTYAVAG--VVSYPEDTVARR 237
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db      352  IDLAYVETL-----KNTWMLORYAVNSADPGVFYLLACGTISSTCGOLASTYPLATVYTR 404
Oy      238  MMMSGKRGKADIYGTGYDQWKRIPKIPDESGKFAFGKASNYLRGAGAFV--LYLYDELK 295
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db      405  MDAQASTIEGAPETVMSL--FKQILITBEAFGLYIGLAPNEKFAIPLAVASIVSYENIK 461

```

RESULT 8
 US-09-482-273-118
 ; Sequence 118, Application US/09482273
 ; Patent No. 6534631
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 71 Human Secreted Proteins
 ; FILE REFERENCE: P2030P1
 ; CURRENT APPLICATION NUMBER: US/09/482,273
 ; CURRENT FILING DATE: 2000-01-13
 ; EARLIER APPLICATION NUMBER: PCV/US99/15849
 ; EARLIER FILING DATE: 1999-07-14
 ; EARLIER APPLICATION NUMBER: 60/092,921

```

: EARLIER FILING DATE: 1998-07-15
: EARLIER APPLICATION NUMBER: 60/092,922
: EARLIER FILING DATE: 1998-07-15
: EARLIER APPLICATION NUMBER: 60/092,956
: EARLIER FILING DATE: 1998-07-15
: NUMBER OF SEQ ID NOS: 267
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 118
: LENGTH: 335
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (335)
: OTHER INFORMATION: xaa equals stop translation
DS-09-482-273-118

```

Query Match	18.58%	Score 286;	DB 4;	length 335;
Best Local Similarity	29.08%	Pred. No. 6.9e-24;		
Matches	87;	Conservative	50;	Mismatches 133;
			Indels	30;
			Gaps	8;

[illegible]

```

RESULT 9
US-09-501-558-2
; Sequence 2, Application US/09501558
; Patent No. 6403784
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6403784e1 Human Uncoupling Proteins and
; TITLE OF INVENTION: polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0012-USA
; CURRENT APPLICATION NUMBER: US/09/501,558
; CURRENT FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-501-558-2

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Query Match	18.4%	Score 283.5;	DB 4,	length 291;
Best Local Similarity	28.9%	Pred. No. 1.1e-23;		
Matches 87;	Conservative 54;	Mismatches 129;	Indels 31;	Gaps 9;

0y 10 KDFLAGGAAAIISKRAVPIERVKLLLOVHNS-----KOIADQYGIYDCIARIKE 64
 0y 11 :
 Db 7 KPFEVGGIASTAECEFTPIDTKTRLDIOGOTNAKKREI----RYGMGLHALVRIRE 62
 0y 65 QGVLSFWRGNTANIRYPPTOALNFAFKDKTKQIFLGVDKHDTQFWRFYAGNLASGANG 124

Db 63 EGIKALYSGLAPAMLRQASGYETKIKGTYSGLRLFIETPERDET-----LPIVNICGILSG 117

QY 125 ATSLCFYPLDFAETRLADYDCKSGTGEREFRLGSCYLTKRKSDGIRGLYGGFSVYOGI 184

Db 118 VIISTIANPYDLVKIKMQA---QSNITQ---GGMIGNFNMTYQOEBOTRLMKMGVSLTQORA 172

QY 185 IYRAATFGYDPAK-----GMLEDPKTKHLYVSMWIAQYTVTAAGVSYSTPEPTVRRM 238

Db 173 AIYVVGELPYDITKTHLLISGLMGDTYTHFLSSF---TCGLAGALASNPVNVYETRM 228

QY 239 MMOSG-RKGAADIYTGTVDCWRRIFREDGKAFFGKAGSNVLR-GMGAFVLVLYDELK 266

Db 229 MNRVLRDGRCSGYTGTLDCLLQTMKNBEGFALYKGFNPWNLRLGPNNIIIFEVYEDLKK 288

QY 297 V 297

Db 289 L 289

```

RESULT 10
US-09-160-119-4
: Sequence 4, Application US/09160119A
: Patent No. 6316219
: GENERAL INFORMATION:
: APPLICANT: KRIEF, STEPHANE
: APPLICANT: SODCHET, MICHEL
: APPLICANT: BRIL, ANTOINE
: TITLE OF INVENTION: NOVEL COMPOUNDS
: FILE REFERENCE: GH-30985
: CURRENT APPLICATION NUMBER: US/09/160, 119A
: CURRENT FILING DATE: 1998-09-24
: EARLIER APPLICATION NUMBER: EP 97402511.6
: EARLIER FILING DATE: 1997-10-23
: EARLIER APPLICATION NUMBER: EP 98401655.0
: EARLIER FILING DATE: 1998-07-02
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: fastseq for Windows Version 3.0
: SEQ ID NO 4
: LENGTH: 447
: TYPE: PRT
: ORGANISM: HOMO SAPIENS
: US-09-160-119-4

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Query Match	18.1%	Score 280;	DB 4;	Length 447;
Best Local Similarity	27.1%	Pred No. 5.1e-23;		
Matches	80;	Conservative 47;	Mismatches 148;	Indels 20;
			Gaps	6

QY QAIISPKDKDLAGGIAIAISKTAJLVAJLEIRKLLLYQVHAKSOIADKQVGVICDVIPIK 63
Db QVAMSAIYRRGLGSVAGAVGATAVIYPIIDLTKIRMQNQBSTGSFVEMIAKNSFCDFKRYLR 155
QY 64 EGVLSFMRGNLANIYRFPFQALNFAFRKYYKQJEL---GGVDKHQFWRFYAGNIASG 120
Db YESEFGLIYRGLLIPOLLGVAPERAKILTYNDFVRDKFMHKDSVP-----LAAELIAG 207
QY 121 GAAGATSLCFVYPLDEAFRRLADAGKSGSTEEFEFGJGDLCLYTKISDGIKGLYQGFYSV 180
Db 208 GCGAGSQVFTNPLEYVKIRLQV-AGEITTTGPRFSAL-----SVVRDLGGFGITKGGKAC 261
QY 181 VQGIITRYRAYFEGVYDTAGMLPDRKKNHIYVNMIAQTIVAV-AGVASYEPFDTVRRRM 239
Db 262 FLNDIPFSAIYPCYAHKVASFANEDQVSPGSLILAGIALGNPAAISLVYRPADYIKR-- 319
QY 240 MOSGRKGADIMTYGYDCNRKILFRDEGGKAFPKAMSVNLKMGAGAYLVLYIDEL 294
Db 320 LQVAAAGQTTYSGVIDCFRKILREEGKALIMKGGAGAVFSSPQFGVTLITLIEL 374

RESULT 11
US-09-160-119-2
; Sequence 2, Application US/09160119A
; Patent No. 6316219

```

1 GENERAL INFORMATION:
2 APPLICANT: KRIEF, STEPHANE
3 APPLICANT: SOUCHET, MICHEL
4 APPLICANT: BRIT, ANTOINETTE
5 TITLE OF INVENTION: NOVEL COMPOUNDS
6 FILE REFERENCE: 94-30985
7 CURRENT APPLICATION NUMBER: US/09/160,119A
8 CURRENT FILING DATE: 1998-09-24
9 EARLIER APPLICATION NUMBER: EP 97402511.6
10 EARLIER FILING DATE: 1997-10-23
11 EARLIER APPLICATION NUMBER: EP 98401655.0
12 EARLIER FILING DATE: 1998-07-02
13 NUMBER OF SEQ ID NOS: 4
14 SOFTWARE: FASTSEQ for Windows Version 3.0
15 SEQ ID NO 2
16 LENGTH: 674
17 TYPE: PRN
18 ORGANISM: HOMO SAPIENS
19 US-03-100-119-2

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Query Match	18.1%	Score 280;	DB 4;	Length 674;
Best Local Similarity	27.1%	Pred. No. 9.4e-23;		
Matches 80;	Conservative 47;	Mismatches 148;	Indels 20;	Gaps 6

QY 4 QAISEFAKQFELGSGTAAALSKSTAVPDIETVKLLQVQASHKQJLAODKQYKGIYDCIVLRPK 63

Db 323 QVASEAYFEFGSGSAGAAAGATAVPDIDVTKRMQORSTGSEVGLAMTKNSPDCERKYLRL 382

QY 64 EOGVLSFMRGMIANVIRYFPTQALFAFKDKYKQFEL---GGVDENHTQFWRFPAENLNSG 120

Db 383 YEGFEGLIRGLLPOLLOGLAVPEKAKILVNDPEVRDKFMHKDGSVP-----LAAEILAG 434

QY 121 GAAATATSCFYYPLDFAETRLAADNGKSTEREFEFGDCLCYTKIKSDGIRGLYOGFSYS 180

Db 435 GCAGSGOYIFNPDELYKIRQLQV-AGETTTGPRYSAL-----SVYRDLGFEGLIIGAAKAC 488

QY 181 VQGIITTYAAAFGYVIDTAKGMLPDKPKNTHLYVSMKIAQTVTA'-AGVSYSPEDTVYRRMM 239

Db 489 FLRDIPIPSALTFPCCAAHVKAASFANDGQVSPGSLLLAALAGMPPASLVTTPADVTKTR-- 546

QY 240 MQSGRKGAADIMYGTGDCWRRILFRDEGKAFFKGAMSVNLKRGMGAFVLYIDEL 294

Db 547 LQVAAARGQTYTSVGIIDCFRKLILREGGKALMKGAGAVFSSPOFGVTLILYEL 601

```

RESULT 12
US-09-142-565-2
Sequence 2, Application US/09142565A
Patent No. 6187560
GENERAL INFORMATION:
APPLICANT: Lee James Beoley
APPLICANT: Kelly Paine
APPLICANT: Robert James
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30002
CURRENT APPLICATION NUMBER: US/09/142,565A
CURRENT FILING DATE: 1999-06-30
EARLIER APPLICATION NUMBER: 9704551.2
EARLIER FILING DATE: 1997-03-05
EARLIER APPLICATION NUMBER: 9705614.7
EARLIER FILING DATE: 1997-03-18
EARLIER APPLICATION NUMBER: 97305305.1
EARLIER FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 312
TYPE: PRF
ORGANISM: HOMO SAPIEN
US-09-142-565-2

```

Query Match	17.2%;	Score 265;	DB 3;	Length 312;
Best Local Similarity	27.1%;	Pred. No. 1.5e-21;		

Matches 82; Conservative 52; Mismatches 145; Indels 24; Gaps 8;

OY 7 SFARDFLAGGIAAISKTAAPIERVKLLLOVQ--HASKQIAADKQYKIVDCIVRIKRE 64
 DB 12 TMAVFLGAGTACFADLVTFPLDTAKVRLQIQESGQPVATVSAQYRGVMTITLMTBEP 71
 OY 65 QGVLSFMGNLANVIRYPTQALNFAFKDKYKQIFL-GGVDKHTQFMYRFGNINLASGAA 123
 DB 72 EGSPSPYGLVAGLOROMSFASIRIGLDSVKQYVTPGADNSSLTTRILA-----GCCTT 126
 OY 124 GATSCIFVYPLDEFARTRLAADV--GKSGTEREFGRLGCLVKITKSDGIRGLYOGFSVS 181
 DB 127 GAAVTCQPTDVYKAVRQASIHGQPSRSDRKISGTMAYRTIAREEGVRLMKGTLPRT 186
 OY 182 QGIIIRAYFYGYDTAKGMLPDPKNTIIVYSMIAQTVA-----VAGVSYSPDTYRR 236
 DB 187 MRNIVNCAEYVYTDILKEKLLD---YHLTDNFCHEVSAFGAGFCATVVASPDVYKT 243
 OY 237 RMMQSGKRGADIMTGTVDCKRTFFRDEGKAFPKGAMSVLR-GMGAFVLYLYDELK 295
 DB 244 RYM-----NSPPGOYFSPDLCKMKVAGGPTAFYKGTSPSFLRLGSMNVVAFVTEQIK 298
 OY 296 KVI 298
 DB 299 RAL 301

RESULT 13
 US-08-518-878B-56
 ; Sequence 56, Application US/08518878B
 ; Patent No. 5702902
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; TITILE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/518-878B
 ; FILING DATE: 23-AUG-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7853-036
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 56:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 299 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; US-08-518-878B-56

Query Match 16.2%; Score 250.5; DB 1; Length 299;
 Best Local Similarity 24.9%; Pred. No. 66-20;
 Matches 74; Conservative 52; Mismatches 146; Indels 25; Gaps 8;

OY 12 FLAGGIAAISKTAAPIERVKLLLOVQASK--QIADKQYKGIIVDCIVRIKREQVL 68

DB 7 FLAGGTAACIADLITFPDITAKVRLQIQESGQPVATVSAQYRGVMTITLMTBEP 66
 OY 69 SFWRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFMYRFGNINLASGAGATSL 128
 DB 67 SLYNGVLVAGLOROMSFASVIRIGLYDSVKQFYTKG--SEHAS-----IGSRLLASTTGALAV 121
 OY 129 CFVYPLDEFARTRLAADVSGTEREFGRLGCLVKITKSDGIRGLYOGFSVSOGIIYR 188
 DB 122 AVAQPTDVYKAVRQAO--ARAGGRRYOSTVNAKYRTIAREEGVRLMKGTSPVARNALYN 180
 OY 189 AAFVGYDTAK-----GMLPDPKNTIIVYSMIAQTVAAGVSYSPDTYRRMMQOS 242
 DB 181 CAELVYTDILKIDALIKANLMTDLPCHFRSAGAGCFCTVVAS---PVDVYKTRYM--- 233
 OY 243 GRKADIMTGTVDCKRTFFRDEGKAFPKGAMSVLR-GMGAFVLYLYDELKRYI 298
 DB 234 --NSALQYSSAGHALMYLQKEGPRATYKGMPSFLRLGSMNVVAFVTEQIKRAL 288

RESULT 14
 US-08-470-868A-56
 ; Sequence 56, Application US/08470868A
 ; Patent No. 5861485
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis C.
 ; TITLE OF INVENTION: Compositions and Methods for the
 ; TITILE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie and Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/470,868A
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7853-0031-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-8864
 ; TELEX: 66441 PENNIE
 ; INFORMATION FOR SEQ ID NO: 56:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 299 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; US-08-470-868A-56

Query Match 16.2%; Score 250.5; DB 2; Length 299;
 Best Local Similarity 24.9%; Pred. No. 66-20;
 Matches 74; Conservative 52; Mismatches 146; Indels 25; Gaps 8;

OY 12 FLAGGIAAISKTAAPIERVKLLLOVQASK--QIADKQYKGIIVDCIVRIKREQVL 68
 DB 7 FLAGGTAACIADLITFPDITAKVRLQIQESGQPVATVSAQYRGVMTITLMTBEP 66
 OY 69 SFWRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFMYRFGNINLASGAGATSL 128
 DB 67 SLYNGVLVAGLOROMSFASVIRIGLYDSVKQFYTKG--SEHAS-----IGSRLLASTTGALAV 121

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 19:38:56 ; Search time 19.355 Seconds

(Without alignments)
2105.969 Million cell updates/sec

Title: US-09-811-132-33

Perfect score: 1543
Sequence: 1 MTEQAISFADFLAGIATAA.....LRGNGAFVLYDELKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 510680 seqs, 136781880 residues

Total number of hits satisfying chosen parameters: 510680

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCR_NEW_PUB.pep:*
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- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1543	100.0	298	9	US-09-811-094-33
2	1543	100.0	298	9	US-09-810-644-33
3	1543	100.0	298	10	US-09-185-904A-33
4	1454	94.2	298	9	US-09-811-094-32
5	1454	94.2	298	9	US-09-810-644-32
6	1454	94.2	298	10	US-09-185-904A-32
7	1385.5	89.8	297	9	US-09-811-094-31
8	1385.5	89.8	297	9	US-09-810-644-31
9	1385.5	89.8	297	9	US-09-185-904A-31
10	760.5	49.3	318	10	US-09-801-368-252
11	749.5	48.6	386	9	US-09-734-569-170
12	737	47.8	308	15	US-10-128-714-3338
13	737	47.8	308	15	US-10-128-714-8338
14	734.5	47.6	381	12	US-10-141-478A-2
15	686	44.5	677	12	US-10-259-165-192

16	518	33.6	132	9	US-09-925-301-1459	Sequence 1459, Ap
17	423	27.4	87	9	US-09-864-761-36440	Sequence 36440, A
18	368	23.8	475	10	US-09-777-921A-2	Sequence 4, Appl1
19	368	23.8	477	10	US-09-777-921A-2	Sequence 2, Appl1
20	333.5	21.6	410	10	US-09-777-921A-5	Sequence 5, Appl1
21	314	20.3	469	9	US-09-989-722-289	Sequence 289, App
22	314	20.3	469	9	US-09-989-722-289	Sequence 289, App
23	314	20.3	469	9	US-09-989-722-289	Sequence 289, App
24	314	20.3	469	9	US-09-989-722-289	Sequence 289, App
25	314	20.3	469	9	US-09-989-722-289	Sequence 289, App
26	314	20.3	469	10	US-09-989-732-289	Sequence 289, App
27	314	20.3	469	10	US-09-991-073-289	Sequence 289, App
28	314	20.3	469	10	US-09-990-442-289	Sequence 289, App
29	314	20.3	469	10	US-09-991-163-289	Sequence 289, App
30	314	20.3	469	10	US-09-993-604-289	Sequence 289, App
31	314	20.3	469	10	US-09-990-444-289	Sequence 289, App
32	314	20.3	469	10	US-09-988-721-289	Sequence 289, App
33	314	20.3	469	10	US-09-992-558-289	Sequence 289, App
34	314	20.3	469	10	US-09-988-293A-289	Sequence 289, App
35	314	20.3	469	10	US-09-988-735-289	Sequence 289, App
36	314	20.3	469	10	US-09-990-444-289	Sequence 289, App
37	314	20.3	469	10	US-09-991-181-289	Sequence 289, App
38	314	20.3	469	10	US-09-988-730-289	Sequence 289, App
39	314	20.3	469	10	US-09-990-436-289	Sequence 289, App
40	314	20.3	469	10	US-09-993-687-289	Sequence 289, App
41	314	20.3	469	11	US-09-989-734-289	Sequence 289, App
42	314	20.3	469	11	US-09-997-653-289	Sequence 289, App
43	314	20.3	469	11	US-09-993-667-289	Sequence 289, App
44	314	20.3	469	11	US-09-997-428-289	Sequence 289, App
45	314	20.3	469	11	US-09-997-666-289	Sequence 289, App

ALIGNMENTS

RESULT 1
US-09-811-094-33
Sequence 33, Appl
Patent No. US2001004414A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-811-094-33

Query Match 100.0% Score 1543; DB 9; Length 298;
Best Local Similarity 100.0% Pred. No. 7.6e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MTEQAISFADFLAGIATAAISKTAIVAPLERKLLQVHASKQIAADKQYGVDCIYR 60
QY 61 IKREGGVLSFWNGNLANVIRFPPTQALNFAFDKQIKQITLGVDKHTQWRFPAGNLSG 120
DB 61 IKREGGVLSFWNGNLANVIRFPPTQALNFAFDKQIKQITLGVDKHTQWRFPAGNLSG 120

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Db      181 VOGIITIRAAVFGYVDPAKGMPLDPKNTHTVSWMIQOTYAAVGVSYFPDYVRRMM 240
      181 VOGIITIRAAVFGYVDPAKGMPLDPKNTHTVSWMIQOTYAAVGVSYFPDYVRRMM 240
QY      241 QSGRKADIMYTGTVDCWKRIFRDEGKAFKFGAMSVNLKMGCAFVLVLYDELKVI 298
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RESULT 2
US-09-810-644-33
; Sequence 33, Application US/09810644
; Patent No. US20020012992A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Willey, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yazhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.4203
; CURRENT APPLICATION NUMBER: US/09/810.644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 298
; TYPE: PRF
; ORGANISM: Homo sapien
; US-09-810-644-33

Query Match      100.0%; Score 1543; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 7.6e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      181 VOGIITIRAAVFGYVDPAKGMPLDPKNTHTVSWMIQOTYAAVGVSYFPDYVRRMM 240
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Db      181 VOGIITIRAAVFGYVDPAKGMPLDPKNTHTVSWMIQOTYAAVGVSYFPDYVRRMM 240
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RESULT 3
US-09-185-904A-33
; Sequence 33, Application US/09185904A
; Patent No. US2002017185A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.

```

```

; APPLICANT: Clevenger, William
; APPLICANT: Willey, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
; TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
; FILE REFERENCE: 660088.420
; CURRENT APPLICATION NUMBER: US/09/185.904A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 298
; TYPE: PRF
; ORGANISM: Homo sapien
; US-09-185-904A-33

Query Match      100.0%; Score 1543; DB 10; Length 298;
Best Local Similarity 100.0%; Pred. No. 7.6e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      181 VOGIITIRAAVFGYVDPAKGMPLDPKNTHTVSWMIQOTYAAVGVSYFPDYVRRMM 240
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RESULT 4
US-09-811-094-32
; Sequence 32, Application US/09811094
; Patent No. US2001004414A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Willey, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yazhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.4204
; CURRENT APPLICATION NUMBER: US/09/811.094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRF
; ORGANISM: Homo sapien
; US-09-811-094-32

Query Match      94.2%; Score 1454; DB 9; Length 298;
Best Local Similarity 92.6%; Pred. No. 2.6e-147;

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Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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DB 1 MTDALSPAKDFLAGGVAIAISKTAVAPIERVKLLQVHASKQIADKQYKGIIDCVRR 60
OY 61 IPKEQGVLSFWRGNLANYIRFPQALNFAFKDKYKQJFLGVDKHTQFWRFAGNLSAG 120
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 IPKEQGVLSFWRGNLANYIRFPQALNFAFKDKYKQJFLGVDKHTQFWRFAGNLSAG 120
OY 121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGDCLVTKRSGIRGLYOGFSYS 180
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGDCLVTKRSGIRGLYOGFSYS 180
OY 181 VOGIIIRAAVFGYVDATKAGMLPDPKNTNHIYVSMIAQTVAVAGVSPFDTVRRMM 240
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 VOGIIIRAAVFGYVDATKAGMLPDPKNTNHIYVSMIAQTVAVAGVSPFDTVRRMM 240
OY 241 OSGRKADIMYTGTDCKRKIFRDEGKAFKAGMSNVLKMGAFVLVLYDELK 296
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 OSGRKGTIDIMYTGTDCKRKIARDEGKAFKAGMSNVLKMGAFVLVLYDELK 296

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RESULT 5

US-09-810-644-32
 ; Sequence 32, Application US/09810644
 ; Patent No. US20020012992A1
 ; GENERAL INFORMATION:

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; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yazhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810,644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-810-644-32

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Query Match 94.2%; Score 1454; DB 9; Length 298;
 Best Local Similarity 92.6%; Pred. No. 2,6e-147;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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OY 1 MTEQAISPAKDFLAGGIAAIAISKTAVAPIERVKLLQVHASKQIADKQYKGIYDCIVR 60
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DB 1 MTDALSPAKDFLAGGVAIAISKTAVAPIERVKLLQVHASKQIADKQYKGIIDCVRR 60
OY 61 IPKEQGVLSFWRGNLANYIRFPQALNFAFKDKYKQJFLGVDKHTQFWRFAGNLSAG 120
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 IPKEQGVLSFWRGNLANYIRFPQALNFAFKDKYKQJFLGVDKHTQFWRFAGNLSAG 120
OY 121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGDCLVTKRSGIRGLYOGFSYS 180
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGDCLVTKRSGIRGLYOGFSYS 180
OY 181 VOGIIIRAAVFGYVDATKAGMLPDPKNTNHIYVSMIAQTVAVAGVSPFDTVRRMM 240
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 VOGIIIRAAVFGYVDATKAGMLPDPKNTNHIYVSMIAQTVAVAGVSPFDTVRRMM 240
OY 241 OSGRKADIMYTGTDCKRKIFRDEGKAFKAGMSNVLKMGAFVLVLYDELK 296
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 OSGRKGTIDIMYTGTDCKRKIARDEGKAFKAGMSNVLKMGAFVLVLYDELK 296

```

RESULT 6

US-09-185-904A-32
 ; Sequence 32, Application US/09185904A
 ; Patent No. US20020177185A1
 ; GENERAL INFORMATION:

```

; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
; TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
; FILE REFERENCE: 660088.420
; CURRENT APPLICATION NUMBER: US/09/185,904A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-185-904A-32

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Query Match 94.2%; Score 1454; DB 10; Length 298;
 Best Local Similarity 92.6%; Pred. No. 2,6e-147;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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OY 1 MTEQAISPAKDFLAGGIAAIAISKTAVAPIERVKLLQVHASKQIADKQYKGIYDCIVR 60
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MTDALSPAKDFLAGGVAIAISKTAVAPIERVKLLQVHASKQIADKQYKGIIDCVRR 60
OY 61 IPKEQGVLSFWRGNLANYIRFPQALNFAFKDKYKQJFLGVDKHTQFWRFAGNLSAG 120
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 IPKEQGVLSFWRGNLANYIRFPQALNFAFKDKYKQJFLGVDKHTQFWRFAGNLSAG 120
OY 121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGDCLVTKRSGIRGLYOGFSYS 180
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGDCLVTKRSGIRGLYOGFSYS 180
OY 181 VOGIIIRAAVFGYVDATKAGMLPDPKNTNHIYVSMIAQTVAVAGVSPFDTVRRMM 240
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 VOGIIIRAAVFGYVDATKAGMLPDPKNTNHIYVSMIAQTVAVAGVSPFDTVRRMM 240
OY 241 OSGRKADIMYTGTDCKRKIFRDEGKAFKAGMSNVLKMGAFVLVLYDELK 296
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 OSGRKGTIDIMYTGTDCKRKIARDEGKAFKAGMSNVLKMGAFVLVLYDELK 296

```

RESULT 7

US-09-811-094-31
 ; Sequence 31, Application US/09811094
 ; Patent No. US20010044144A1
 ; GENERAL INFORMATION:

```

; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yazhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37

```


APPLICANT: Moughamer, Todd
APPLICANT: Provart, Nicholas
APPLICANT: Rlicke, Darrell
TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
FILE REFERENCE: 70030-NP
CURRENT APPLICATION NUMBER: US/10/259,165
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/368,327
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 782
SOFTWARE: Patentlist.pl version 3.0.4 (C) 2001 Syngenta
SEQ ID NO 192
LENGTH: 677
TYPE: PRT
ORGANISM: Oryza sativa
US-10-259-165-192

Query Match 44.5%; Score 686; DB 12; Length 677;

Best Local Similarity 50.3%; Pred. No. 1.4e-64;

Matches 155; Conservative 43; Mismatches 86; Indels 22; Gaps 9;

QY 3 EQAIS-FAKDELAGIAAISKTAIVAPLERVKLLQVQ-HASKQIADKQYKIVDCIVR 60
DB 370 EKGISGFMDPMGVSAAVSKTAAPIERIKLIONDEMIKSGRLSHPKGIADCRGR 429
QY 61 IPKQGVLSFTRGMLANYIRFPTQALNFAFKDKYKQIFLGVNDKHTQFMRYFAGNLASG 120
DB 430 TINDEGVIALMRGTANYIRFPTQALNFAFKDHFRRMFNFKKDK-DGYMKWFAGNLASG 488
QY 121 GAAGATSLCFYPPDEAFRTLAAD-VKSGTEREPRGIDGCIIVTKRSDGIRGLY---Q 175
DB 489 GAAGACSLFEFYSLDIARTRLANDAKAAKKGGRFNGLDVYRRTLASDGIAGLTPWIQ 548
QY 176 GFSVSVQGIITRYAAYEGVDYAK---GMLPDPKNTHTIYVSWMIQTVTAVAGVSY 230
DB 549 HLPVLYS--LSNRGLYGMVDSLKPVLVGNLQD---NFLASFLGNGITIGAGLASYP 602
QY 231 FDTYRRRMMQSGRKGADIMTGTVCWRKIFRDEGGAFFKGAWSNVLKMGAGFVLVL 290
DB 603 IDTYRRRMMTSGEA--VKYNSSIDAFKQIVAKGAKSLFKGAGANILRAVAGAVLAG 659
QY 291 YDELKVI 298
DB 660 YDKLQVVV 667

Search completed: August 28, 2003, 19:45:25
Job time : 20.355 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 19:35:01 ; Search time 20.6898 Seconds

(without alignments)
1385.139 Million cell updates/sec

Title: US-09-811-132-33

Perfect score: 1543

Sequence: 1 MTEQAISFADFLAGIAA.....LRGNGAFVLVYDELKKVI 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	1	S03894 ADP,ATP carrier pr
2	1512	98.0	298	1	B43646 ADP,ATP carrier pr
3	1454	94.2	298	1	A29132 ADP,ATP carrier pr
4	1424	92.3	298	1	I60173 adenine nucleotide
5	1422	92.2	298	1	XWBO ADP,ATP carrier pr
6	1418	91.9	298	1	S37210 ADP,ATP carrier pr
7	1409	91.3	298	1	A44778 ADP,ATP carrier pr
8	1405	91.1	298	1	S31814 ADP,ATP carrier pr
9	1184	76.7	301	1	S31935 ADP,ATP carrier pr
10	1041	67.5	313	2	T23207 hypothetical prote
11	1039	67.3	313	2	T23850 hypothetical prote
12	1038	67.3	300	2	T25371 hypothetical prote
13	993.5	64.4	300	2	T15206 hypothetical prote
14	978	63.4	339	2	A41677 ADP,ATP carrier pr
15	943	61.1	301	2	S51132 ADP,ATP carrier pr
16	778.5	50.5	307	2	A36582 ADP,ATP carrier pr
17	772	50.0	308	1	S30259 ADP,ATP carrier pr
18	769	49.8	322	2	T40526 adp,atp translocas
19	768	49.8	386	2	T09709 ADP,ATP carrier pr
20	766	49.6	313	1	XWNC ADP,ATP carrier pr
21	764	49.5	326	2	T25728 hypothetical prote
22	762.5	49.4	305	2	S68154 ADP,ATP carrier pr
23	760.5	49.3	318	1	A31978 ADP,ATP carrier pr
24	756.5	49.0	306	2	T20012 hypothetical prote
25	750	48.6	387	2	S14876 ADP,ATP carrier pr
26	748	48.5	386	2	S21974 ADP,ATP carrier pr
27	747	48.4	306	2	T42011 ADP,ATP carrier pr
28	747	48.4	386	2	S17917 ADP,ATP carrier pr
29	744	48.2	387	2	S16568 ADP,ATP carrier pr

30	743	48.2	379	2	T04608 ADP,ATP carrier pr
31	742.5	48.1	385	1	S29852 ADP,ATP carrier pr
32	742	48.1	382	2	S33630 ADP,ATP carrier pr
33	739.5	47.9	386	2	S14874 ADP,ATP carrier pr
34	737.5	47.8	309	2	A24849 ADP,ATP carrier pr
35	734.5	47.6	379	2	S21313 ADP,ATP carrier pr
36	681.5	44.2	298	2	T24029 ADP,ATP translocas
37	520.5	33.7	327	2	T51577 ADP,ATP translocas
38	383	24.8	325	2	T04273 hypothetical prote
39	381	24.7	352	2	T01729 mitochondrial solu
40	372	24.1	358	2	T45934 hypothetical prote
41	370.5	24.0	415	2	T48171 hypothetical prote
42	369.5	23.9	381	2	T51158 hypothetical prote
43	368	23.8	475	2	T50686 peroxisomal Ca-dep
44	363	23.5	348	2	D84798 probable mitochond
45	344.5	22.3	332	2	T47703 Ca-dependent solut

ALIGNMENTS

RESULT 1

S03894
ADP,ATP carrier protein T3 - human
N:Alternate names: ADP,ATP carrier protein T2 (misidentification); mitochondrial ADP,
C:Species: Homo sapiens (man)
C>Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C:Accession: S03894; B28116
R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A>Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP
A:Reference number: S03893; MUID:89236396; PMID:2541251
A:Accession: S03894
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-298 <CO2>
R:Holdsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A>Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
A:Reference number: A94197; MUID:88124845; PMID:2829183
A:Accession: B28116
A:Molecule type: mRNA
A:Residues: 36-104, 'R', 106, 'A', 109-298 <HO2>
A:Cross-References: GB:J03592; NID:9339722; PIDN:AAA36750.1; PID:9339723
A:Experimental source: liver
A:Genetics:
A:Gene: GDB:ANT3; ANT3Y
A:Cross-References: GDB:125184; OMIM:300151; OMIM:403000
A:Map position: xp22.32-xp22.32; yp11.3-yp11.3
A>Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology.
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:2-268/Product: ADP,ATP carrier protein status predicted <ANT>
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 100.0%; Score 1543; DB 1; Length 298;

Best Local Similarity 100.0%; Pred. No. 6e-129;

Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTEQAISFADFLAGIAAISKTAAPFERKLLIQVOHASKQIADROYGIYDCIYR	60
DB	1	MTEQAISFADFLAGIAAISKTAAPFERKLLIQVOHASKQIADROYGIYDCIYR	60
QY	61	IRKEGVLSFWRGNLANVIRFPPTQALNFAFDKRYKQIFLGVDKHTQFWRYFAGNIASG	120
DB	61	IRKEGVLSFWRGNLANVIRFPPTQALNFAFDKRYKQIFLGVDKHTQFWRYFAGNIASG	120
QY	121	GAAGATSCFVYPLDFARTRLAADVGSSTEEFEFGICVYKTRSDGIRLQGFSSVS	180
DB	121	GAAGATSCFVYPLDFARTRLAADVGSSTEEFEFGICVYKTRSDGIRLQGFSSVS	180

QY 181 VGGIIIRAAVFEGVDTAKGMLDPKNTHTVSMIAQTATVAVGVSTPFDVRRMM 240
 |||||
 Db 181 VGGIIIRAAVFEGVDTAKGMLDPKNTHTVSMIAQTATVAVGVSTPFDVRRMM 240
 QY 241 QSGRKADIMYGTGTVDCWKRIKIFDEGKAFKFGKAMSNVLRGMGAFVLVLYDELKRYI 298
 |||||
 Db 241 QSGRKADIMYGTGTVDCWKRIKIFDEGKAFKFGKAMSNVLRGMGAFVLVLYDELKRYI 298

RESULT 2

B43646
 ADP,ATP carrier protein T2 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
 C:Accession: B43646
 R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989
 A>Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MIM:89229093; PMID:2540808
 A:Accession: B43646
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <POM>
 A:Cross-references: GB:M24103; NID:9529416; PIDN:AAA30769.1; PID:9529417
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 98.0%; Score 1512; DB 2; Length 298;
 Best Local Similarity 97.7%; Pred. No. 3.3e-126;
 Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTEQATSPKDFLAGGIAAISTKVAPIERVKLLQVGHASQIADKQKGIYDCYR 60
 |||||
 Db 1 MTEQATSPKDFLAGGIAAISTKVAPIERVKLLQVGHASQIADKQKGIYDCYR 60
 QY 61 IPEQGVLSFWRGNLANVIRYPTQALNFAKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 |||||
 Db 61 IPEQGVLSFWRGNLANVIRYPTQALNFAKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPAKRLADVGKSGFEREGIDGLVYITKSDGRGLYOGFNS 180
 |||||
 Db 121 GAAGATSLCFVYPLDPAKRLADVGKSGFEREGIDGLVYITKSDGRGLYOGFNS 180
 QY 181 VGGIIIRAAVFEGVDTAKGMLDPKNTHTVSMIAQTATVAVGVSTPFDVRRMM 240
 |||||
 Db 181 VGGIIIRAAVFEGVDTAKGMLDPKNTHTVSMIAQTATVAVGVSTPFDVRRMM 240
 QY 241 QSGRKADIMYGTGTVDCWKRIKIFDEGKAFKFGKAMSNVLRGMGAFVLVLYDELKRYI 298
 |||||
 Db 241 QSGRKADIMYGTGTVDCWKRIKIFDEGKAFKFGKAMSNVLRGMGAFVLVLYDELKRYI 298

RESULT 3

A29132
 ADP,ATP carrier protein T2 - human
 N:Alternate names: mitochondrial ADP,ATP translocase 2
 C:Species: Homo sapiens (man)
 C>Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C:Accession: A29132; C28116
 R:Bactini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.
 J. Biol. Chem. 262, 4355-4359, 1987
 A>Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulated
 A:Reference number: A29132; MIM:87166056; PMID:3031073
 A:Accession: A29132
 A:Molecule type: mRNA
 A:Residues: 1-298 <RAT>
 A:Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247
 R:Houldsworth, J.; Altardi, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A>Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in d

A:Reference number: A94197; MIM:86124845; PMID:2829183
 A:Accession: C28116
 A:Molecule type: mRNA
 A:Residues: 47-65,'G','67-110','L','112-161','G','163-298 <HOU>
 A:Cross-references: GB:J03591; NID:g339720; PIDN:AAA36749.1; PID:g339721
 A:Experimental source: clone PHAT3
 C:Genetics:
 A:Gene: GDB:ANT2; T3; 2F1
 A:Cross-references: GDB:125190; OMIM:300150
 A:Map position: Xq13-Xq26
 A>Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1454; DB 1; Length 298;
 Best Local Similarity 92.6%; Pred. No. 4.5e-121;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQATSPKDFLAGGIAAISTKVAPIERVKLLQVGHASQIADKQKGIYDCYR 60
 |||||
 Db 1 MTEQATSPKDFLAGGIAAISTKVAPIERVKLLQVGHASQIADKQKGIYDCYR 60
 QY 61 IPEQGVLSFWRGNLANVIRYPTQALNFAKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 |||||
 Db 61 IPEQGVLSFWRGNLANVIRYPTQALNFAKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPAKRLADVGKSGFEREGIDGLVYITKSDGRGLYOGFNS 180
 |||||
 Db 121 GAAGATSLCFVYPLDPAKRLADVGKSGFEREGIDGLVYITKSDGRGLYOGFNS 180
 QY 181 VGGIIIRAAVFEGVDTAKGMLDPKNTHTVSMIAQTATVAVGVSTPFDVRRMM 240
 |||||
 Db 181 VGGIIIRAAVFEGVDTAKGMLDPKNTHTVSMIAQTATVAVGVSTPFDVRRMM 240
 QY 241 QSGRKADIMYGTGTVDCWKRIKIFDEGKAFKFGKAMSNVLRGMGAFVLVLYDELKRYI 298
 |||||
 Db 241 QSGRKADIMYGTGTVDCWKRIKIFDEGKAFKFGKAMSNVLRGMGAFVLVLYDELKRYI 298

RESULT 4

I60173
 adenine nucleotide translocator - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
 C:Accession: I60173
 R:Shiohara, Y.; Kamada, M.; Yamazaki, N.; Terada, H.
 Blochim. Biophys. Acta 1152, 192-196, 1993
 A>Title: Isolation and characterization of cDNA clones and a genomic clone encoding r
 A:Reference number: I60173; MIM:94002161; PMID:8399300
 A:Accession: I60173
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-298 <RES>
 A:Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA43842.1; PID:g400427
 C:Genetics:
 A:Gene: ant1
 A:Introns: 37/3; 200/1; 247/1
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 92.3%; Score 1424; DB 2; Length 298;
 Best Local Similarity 89.6%; Pred. No. 2e-118;
 Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQATSPKDFLAGGIAAISTKVAPIERVKLLQVGHASQIADKQKGIYDCYR 60
 |||||
 Db 1 MTEQATSPKDFLAGGIAAISTKVAPIERVKLLQVGHASQIADKQKGIYDCYR 60


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OY 61 IPKEGVLSFWRGNLANVIRYPTQALNFAEKDKYKQIFLGVDKHTQFWRFPAGNLASG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 IPKEGVLSFWRGNLANVIRYPTQALNFAEKDKYKQIFLGVDKHTQFWRFPAGNLASG 120
OY 121 GAAGATSLCEFYVPLDPFARTRLAADVKGSGTEREFGGLDCLVKTKRSGIKGLYGFVS 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 GAAGATSLCEFYVPLDPFARTRLAADVKGSGTEREFGGLDCLVKTKRSGIKGLYGFVS 180
OY 181 VGGIITRYAAAYGVYDFAKGLPDPKRNTHIVSMIAQVTVAAGVSYPTVRRMM 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 VGGIITRYAAAYGVYDFAKGLPDPKRNTHIVSMIAQVTVAAGVSYPTVRRMM 240
OY 241 OSGRGADIMYTGTVDCWKRIKDEGKRAFFKGAMSNVLRGMAFVLYLDELKRYI 298
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 OSGRGADIMYTGTVDCWKRIKDEGKRAFFKGAMSNVLRGMAFVLYLDELKRYI 298

RESULT 5
XMO
ADP,ATP carrier protein T1 - bovine
N:Alternate names: ADP/ATP translocase T1
C:Species: Bos primigenius taurus (cattle)
C>Date: 14-Nov-1993 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999
C:Accession: A43646; A24822; A03181; A61343; S69369
R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 1989
A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
A:Reference number: A43646; MUID:89229093; PMID:2540808
A:Accession: A43646
A:Molecule type: mRNA
A:Residues: 1-298 <POM>
R:Rasmussen, U.B.; Mohlirab, H.
Biochem. Biophys. Res. Commun. 138, 850-857, 1986
A:Title: Bovine cardiac mitochondrial ADP/ATP carrier: two distinct mRNAs and an unusual
A:Reference number: A24822; MUID:86295775; PMID:3017341
A:Accession: A24822
A:Molecule type: mRNA
A:Residues: 208-298 <RAS>
R:Rasmussen, U.B.; Mohlirab, H.
Biochem. Biophys. Res. Commun. 138, 850-857, 1986
A:Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondrion
A:Reference number: A03181; MUID:82188267; PMID:7076130
A:Accession: A03181
A:Molecule type: protein
A:Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298 <MO>
A:Note: residue 52 may be methyllysine
R:Babel, W.; Wachter, E.; Aquila, H.; Klungenberg, M.
Biochim. Biophys. Acta 670, 176-180, 1981
A:Title: Amino acid sequence determination of the ADP,ATP carrier from beef heart mitoch
A:Reference number: A61343; MUID:82046808; PMID:6271240
A:Accession: A61343
A:Molecule type: protein
A:Residues: 205-298 <BAB>
R:Oetmeier, W.; Masson, K.; Kalina, S.
Eur. J. Biochem. 227, 730-733, 1995
A:Title: [(3)H]7-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP
A:Reference number: S69369; MUID:95172058; PMID:7867632
A:Accession: S69369
A:Molecule type: protein
A:Residues: 49-63;154-168 <OET>
C:Comment: This protein is synthesized in the cytosol and transported into the mitochond
C:Complex: homodimer
C:Function:
A:Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera
A:Note: located in the inner mitochondrial membrane
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitoch
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

```

```

F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
F:52/Modified site: N6-methyllysine (Lys) #status predicted
Query Match 92.2%; Score 1422; DB 1; Length 298;
Best Local Similarity 89.3%; Pred. No. 3,1e-118;
Matches 265; Conservative 19; Mismatches 13; Indels 0; Gaps 0;
OY 1 MTEQAISPAKDFLAGIAAISTKTAVERKLLIQVHASKQJAAADKQYGIYDCYR 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MSDQALSLKDFLAGIAAISTKTAVERKLLIQVHASKQJAAADKQYGIYDCYR 60
OY 61 IPKEGVLSFWRGNLANVIRYPTQALNFAEKDKYKQIFLGVDKHTQFWRFPAGNLASG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 IPKEGVLSFWRGNLANVIRYPTQALNFAEKDKYKQIFLGVDKHTQFWRFPAGNLASG 120
OY 121 GAAGATSLCEFYVPLDPFARTRLAADVKGSGTEREFGGLDCLVKTKRSGIKGLYGFVS 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 GAAGATSLCEFYVPLDPFARTRLAADVKGSGTEREFGGLDCLVKTKRSGIKGLYGFVS 180
OY 181 VGGIITRYAAAYGVYDFAKGLPDPKRNTHIVSMIAQVTVAAGVSYPTVRRMM 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 VGGIITRYAAAYGVYDFAKGLPDPKRNTHIVSMIAQVTVAAGVSYPTVRRMM 240
OY 241 OSGRGADIMYTGTVDCWKRIKDEGKRAFFKGAMSNVLRGMAFVLYLDELKRYI 298
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 OSGRGADIMYTGTVDCWKRIKDEGKRAFFKGAMSNVLRGMAFVLYLDELKRYI 298

RESULT 6
S37210
ADP,ATP carrier protein T1 - mouse
N:Alternate names: adenine nucleotide carrier
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
C:Accession: S37210
R:Laplace, C.; Costec, P.
submitted to the EMBL Data Library, September 1993
A:Reference number: S37210
A:Accession: S37210
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-298 <LAP>
R:Rasmussen, U.B.; Mohlirab, H.
Biochem. Biophys. Res. Commun. 138, 850-857, 1986
A:Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondrion
A:Reference number: A03181; MUID:82188267; PMID:7076130
A:Accession: A03181
A:Molecule type: protein
A:Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298 <MO>
A:Note: residue 52 may be methyllysine
R:Babel, W.; Wachter, E.; Aquila, H.; Klungenberg, M.
Biochim. Biophys. Acta 670, 176-180, 1981
A:Title: Amino acid sequence determination of the ADP,ATP carrier from beef heart mitoch
A:Reference number: A61343; MUID:82046808; PMID:6271240
A:Accession: A61343
A:Molecule type: protein
A:Residues: 205-298 <BAB>
R:Oetmeier, W.; Masson, K.; Kalina, S.
Eur. J. Biochem. 227, 730-733, 1995
A:Title: [(3)H]7-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP
A:Reference number: S69369; MUID:95172058; PMID:7867632
A:Accession: S69369
A:Molecule type: protein
A:Residues: 49-63;154-168 <OET>
C:Comment: This protein is synthesized in the cytosol and transported into the mitochond
C:Complex: homodimer
C:Function:
A:Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera
A:Note: located in the inner mitochondrial membrane
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitoch
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
Query Match 91.9%; Score 1418; DB 2; Length 298;
Best Local Similarity 88.9%; Pred. No. 6,9e-118;
Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;
OY 1 MTEQAISPAKDFLAGIAAISTKTAVERKLLIQVHASKQJAAADKQYGIYDCYR 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MSDQALSLKDFLAGIAAISTKTAVERKLLIQVHASKQJAAADKQYGIYDCYR 60
OY 61 IPKEGVLSFWRGNLANVIRYPTQALNFAEKDKYKQIFLGVDKHTQFWRFPAGNLASG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 IPKEGVLSFWRGNLANVIRYPTQALNFAEKDKYKQIFLGVDKHTQFWRFPAGNLASG 120
OY 121 GAAGATSLCEFYVPLDPFARTRLAADVKGSGTEREFGGLDCLVKTKRSGIKGLYGFVS 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 GAAGATSLCEFYVPLDPFARTRLAADVKGSGTEREFGGLDCLVKTKRSGIKGLYGFVS 180
OY 181 VGGIITRYAAAYGVYDFAKGLPDPKRNTHIVSMIAQVTVAAGVSYPTVRRMM 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 VGGIITRYAAAYGVYDFAKGLPDPKRNTHIVSMIAQVTVAAGVSYPTVRRMM 240
OY 241 OSGRGADIMYTGTVDCWKRIKDEGKRAFFKGAMSNVLRGMAFVLYLDELKRYI 298
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 OSGRGADIMYTGTVDCWKRIKDEGKRAFFKGAMSNVLRGMAFVLYLDELKRYI 298

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Db 241 OSGRKADIMYTGTLDCWKRIADKDEGAKAFKGMWSNVLMGGAFLVLYDEIKKY 298

RESULT 7

A44778

ADP, ATP carrier protein T1 - human

N/Alternate names: mitochondrial ADP, ATP translocase 1

C/Species: Homo sapiens (man)

C/Date: 17-Mar-2000 #sequence, revision 17-Mar-2000 #text_change 17-Mar-2000

C/Accession: A44778; S03893; A39891; A28116

R/L: R.; Warner, C.K.; Hodges, J.R.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M.

J. Biol. Chem. 264, 13998-14004, 1989

A/Title: A human muscle adenine nucleotide translocator gene has four exons, is located

A/Reference number: A44778; MUID:89340499; PMID:2547778

A/Accession: A44778

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-298 <LTA>

A/Cross-references: GB:J04982; NID:q178658; PIDN:AAA51736.1; PID:q178659

R/Cozens, A.L.; Runswick, M.J.; Walker, J.E.

J. Mol. Biol. 206, 261-280, 1989

A/Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr

A/Reference number: S03893; MUID:89236396; PMID:2541251

A/Accession: S03893

A/Status: not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 1-298 <CO2>

R/Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.

Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987

A/Title: CDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader

A/Reference number: A39891; MUID:88041149; PMID:2823266

A/Accession: A39891

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 <NEC>

A/Cross-references: GB:J02966; NID:q339919; PIDN:AAA61223.1; PID:q339920

A/Experimental source: clone pHMANT

R/Houlsworth, J.; Attardi, G.

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A/Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a

A/Reference number: A94197; MUID:88124845; PMID:2829183

A/Accession: A28116

A/Molecule type: mRNA

A/Residues: 1-37 <HOU>

A/Cross-references: GB:J03593; NID:q339724; PIDN:AAA36751.1; PID:q339725

A/Experimental source: liver

C/Genetics:

A/Gene: GDB:ANT1; T1

A/Cross-references: GDB:119680; OMIM:103220

A/Map position: 4q35-4q35

C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

C/Keywords: duplication; homodimer; mitochondrion; transmembrane protein

F/2-298/Product: ADP, ATP carrier protein #status predicted <ANT>

F/5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>

F/110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>

F/207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 91.3%; Score 1409; DB 1; Length 298;

Best Local Similarity 88.3%; Pred. No. 4.3e-117;

Matches 263; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTEQATSFADFLAGGIAAISTKAVPIRVRVLLQVQASQIAADKQYKGIIVDCYR 60

Db 1 MGHAAVSFLKDFLAGGVAASVSTAAVPIRVRVLLQVQASQIAADKQYKGIIVDCYR 60

QY 61 IPEQGVLSFWRGNLANVIRYPTQALNFAFKRYKQIFLGVDKHTQFRRYAGNLSG 120

Db 61 IPEQGVLSFWRGNLANVIRYPTQALNFAFKRYKQIFLGVDKHTQFRRYAGNLSG 120

QY 121 GAAGATSLCFVYPLDFARTRLAADVGSKTEREPRGIGDCLVTKITSNGIRGLYOGFSVS 180

Db 121 GAAGATSLCFVYPLDFARTRLAADVGSKTEREPRGIGDCLVTKITSNGIRGLYOGFSVS 180

QY 181 VQGIITIRAAVFGYVDFAKGMLDPKNTHTVSVMTAQVTAAGVSVYDFVRRMM 240

Db 181 VQGIITIRAAVFGYVDFAKGMLDPKNTHTVSVMTAQVTAAGVSVYDFVRRMM 240

QY 241 OSGRKADIMYTGTLDCWKRIADKDEGAKAFKGMWSNVLMGGAFLVLYDEIKKY 298

Db 241 OSGRKADIMYTGTLDCWKRIADKDEGAKAFKGMWSNVLMGGAFLVLYDEIKKY 298

RESULT 8

S31814

ADP, ATP carrier protein T2 - mouse

N/Alternate names: adenine nucleotide translocase

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence, revision 06-Jan-1995 #text_change 09-Apr-1998

C/Accession: S31814

R/Costel, P.; Laplace, C.

submitted to the EMBL Data Library, January 1993

A/Reference number: S31814

A/Accession: S31814

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-298 <COS>

A/Cross-references: EMBL:X70847

C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

C/Keywords: duplication; transmembrane protein

F/5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>

F/110-202/Domain: ADP, ATP carrier protein repeat homology <ACP>

F/207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 91.1%; Score 1405; DB 2; Length 298;

Best Local Similarity 89.2%; Pred. No. 9.8e-117;

Matches 264; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTEQATSFADFLAGGIAAISTKAVPIRVRVLLQVQASQIAADKQYKGIIVDCYR 60

Db 1 MTDAAVSFADFLAGGVAASVSTAAVPIRVRVLLQVQASQIAADKQYKGIIVDCYR 60

QY 61 IPEQGVLSFWRGNLANVIRYPTQALNFAFKRYKQIFLGVDKHTQFRRYAGNLSG 120

Db 61 IPEQGVLSFWRGNLANVIRYPTQALNFAFKRYKQIFLGVDKHTQFRRYAGNLSG 120

QY 121 GAAGATSLCFVYPLDFARTRLAADVGSKTEREPRGIGDCLVTKITSNGIRGLYOGFSVS 180

Db 121 GAAGATSLCFVYPLDFARTRLAADVGSKTEREPRGIGDCLVTKITSNGIRGLYOGFSVS 180

QY 181 VQGIITIRAAVFGYVDFAKGMLDPKNTHTVSVMTAQVTAAGVSVYDFVRRMM 240

Db 181 VQGIITIRAAVFGYVDFAKGMLDPKNTHTVSVMTAQVTAAGVSVYDFVRRMM 240

QY 241 OSGRKADIMYTGTLDCWKRIADKDEGAKAFKGMWSNVLMGGAFLVLYDEIKKY 296

Db 241 OSGRKADIMYTGTLDCWKRIADKDEGAKAFKGMWSNVLMGGAFLVLYDEIKKY 296

RESULT 9

S31935

ADP, ATP carrier protein - African malaria mosquito

C/Species: Anopheles gambiae (African malaria mosquito)

C/Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text_change 10-Sep-1999

C/Accession: S31935; S31936

R/Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H.

submitted to the EMBL Data Library, February 1993

A/Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae

A/Reference number: S31935

A/Accession: S31935

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-301 <BEA>

A/Cross-references: EMBL:Z21814; EMBL:Z21815

C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

C/Keywords: duplication; transmembrane protein

F/7-101/Domain: ADP, ATP carrier protein repeat homology <ACP1>

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 19:28:06 ; Search time 12.0134 Seconds

(without alignments)
1166.524 Million cell updates/sec

Title: US-09-811-132-33

Perfect score: 1543

Sequence: 1 MTEGAISFANDELFLAGIAAA.....LRGNGAFVLVDELKKVI 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	1543	100.0	298 1 ADP3_HUMAN	P12236 homo sapien
2	1512	98.0	298 1 ADP3_BOVIN	P32007 bos taurus
3	1463	94.8	298 1 ADP2_HUMAN	P05141 homo sapien
4	1451	94.0	298 1 ADP2_RAT	Q09073 rattus norv
5	1445	93.6	298 1 ADP2_MOUSE	P51881 mus musculu
6	1424	92.3	298 1 ADP1_RAT	O05962 rattus norv
7	1418	91.9	298 1 ADP1_MOUSE	P46962 mus musculu
8	1417	91.8	297 1 ADP1_BOVIN	P02722 bos taurus
9	1409	91.3	298 1 ADP1_HUMAN	P12235 homo sapien
10	1254.5	81.3	299 1 ADT_ANGA	Q26365 dirosophila
11	1204	78.0	301 1 ADT_ANGA	Q27238 anopheles g
12	978	63.4	339 1 ADT_CHIKE	P31692 chlorella k
13	778.5	50.5	307 1 ADP3_YEAST	P18238 saccharomyc
14	772	50.0	308 1 ADT_CHIRE	P27080 chlamydomon
15	769	49.8	322 1 ADT_SCHPO	Q09188 schizosacch
16	768	49.8	386 1 ADP1_GOSHI	O22342 gossypium h
17	766	49.6	313 1 ADP_NEUCR	P02723 neurospora
18	762.5	49.4	305 1 ADT_KLULA	P49382 kluyveromyc
19	760.5	49.3	318 1 ADP2_YEAST	P18239 saccharomyc
20	750.5	48.6	385 1 ADP2_ARATH	P40941 arabidopsis
21	750	48.6	387 1 ADP1_MAIZE	P04709 zea mays (m
22	748	48.5	386 1 ADT_SOLTU	P31691 solanum tub
23	747	48.4	382 1 ADT_ORYSA	P31691 oryza sativ
24	744	48.2	387 1 ADP2_MAIZE	P12857 zea mays (m
25	742.5	48.1	381 1 ADP1_ARATH	P31167 arabidopsis
26	740	48.0	331 1 ADP1_WHEAT	Q4129 triticum ae
27	739.5	47.9	386 1 ADP2_SOLTU	P27081 saccharomyc
28	737.5	47.8	309 1 ADP1_YEAST	P04710 saccharomyc
29	727	47.1	331 1 ADP2_WHEAT	Q41630 triticum ae
30	305.5	19.8	565 1 CMC3_CAEEL	O19529 caenorhabdt
31	302	19.6	588 1 CMC2_CAEEL	O20799 caenorhabdt
32	300	19.4	330 1 GDC_BOVIN	O01888 bos taurus
33	299	19.4	307 1 ODC2_YEAST	O09297 saccharomyc

34	295	19.1	678 1 CMC1_HUMAN	O75746 homo sapien
35	289.5	18.8	322 1 GDC_RAT	P1261 rattus norv
36	287.5	18.6	702 1 CMC1_CAEEL	O21153 caenorhabdt
37	286	18.5	325 1 UCP5_HUMAN	O95258 homo sapien
38	285	18.5	332 1 GDC_HUMAN	P16260 homo sapien
39	284	18.4	325 1 UCP5_MOUSE	O95262 mus musculu
40	282.5	18.3	326 1 YE08_SCHPO	O13805 schizosacch
41	280	18.1	675 1 CMC2_HUMAN	O94350 homo sapien
42	272	17.6	315 1 MFT_HUMAN	O912d1 homo sapien
43	270	17.5	315 1 SAI8_HUMAN	O911k4 homo sapien
44	265	17.2	312 1 UCP3_HUMAN	P55916 homo sapien
45	265	17.2	676 1 CMC2_MOUSE	O9qxx4 mus musculu

ALIGNMENTS

RESULT 1
ADP3_HUMAN STANDARD; PRT; 298 AA.
AC P12236; Q96C49;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)
DE (Adenine nucleotide translocator 3) (ANT 3).
GN SLC25A6 OR ANT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=89236396; PubMed=2541251;
RX Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
RT ADP/ATP translocase.";
RL J. Mol. Biol. 206:261-280(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
RA Margolin J.F.;
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22386257; PubMed=12477932;
RA Klausner R.D., Feigold E.A., Grouse L.H., Derge J.G.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.D., Malek J.A., Gunaratne P.H.,
RA Villard D.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,
RA Richardson D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.J., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 36-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86124645; PubMed=2829183;
RA Houdsworth J., Altardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA

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RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J03592; AAA36750.1; -
DR EMBL: AY007135; AAC01988.1; -
DR EMBL: BC007295; AAH07295.1; -
DR EMBL: BC007850; AAH07850.1; -
DR EMBL: BC008737; AAH08737.1; -
DR EMBL: BC008935; AAH08935.1; -
DR EMBL: BC014775; AAH14775.1; -
DR PIR: S03894; S03894.
DR Genew: HGNC:10992; SLC25A6.
DR MIM: 300151; -
DR GO: GO:0005744; C:mitochondrial inner membrane translocase co. .; TAS.
DR GO: GO:0005471; F:ATP/ADP antiporter activity; NMS.
DR GO: GO:0006854; P:ATP/ADP exchange; TAS.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR002030; Mlt_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
DR MultiGene family: Inner membrane; Repeat; Transmembrane; Transport;
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 100 1.
FT REPEAT 101 208 2.
FT REPEAT 209 298 3.
FT CONFLICT 105 108 KHTQ -> RHA (in ref. 4).
FT CONFLICT 242 242 S -> F (in ref. 3; AAH14775).
SQ SEQUENCE 298 AA; 32866 MW; 18534E9F0E49672F CRC64;
Query Match 100.0%; Score 1543; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 3.6e-128;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 QSGRKGADIMYTGIVDCWRIIFRDEGKAFFKGAWSVNLKMGAFVLYVDELKKYI 298
DB 241 QSGRKGADIMYTGIVDCWRIIFRDEGKAFFKGAWSVNLKMGAFVLYVDELKKYI 298
RESULT 2
ADT3_BOVIN STANDARD; PRT; 298 AA.
ID ADT3_BOVIN
AC P32007;
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, isoform T2 (ADP/ATP translocase 3) (Adenine
DE nucleotide translocator 3) (ANT 3).
GN SLC25A6 OR ANT3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP MEDLINE=89229093; PubMed=2540808;
RA Powell S.J., Mead S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues."
RL Biochemistry 28:866-873(1989).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M24103; AAA30769.1; -
DR PIR: B43646; B43646.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR002030; Mlt_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
DR MultiGene family: Inner membrane; Repeat; Transmembrane; Transport;
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 2 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32877 MW; 1C34E7DE6E4061 CRC64;
Query Match 98.0%; Score 1512; DB 1; Length 298;
Best Local Similarity 97.7%; Pred. No. 1.9e-125;
Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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OY 61 IPKEGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAQNLASG 120
DB 61 IPKEGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAQNLASG 120
OY 121 GAAGATSLCFYPPDLPARTRLADVGKSGTEREFGDCLVYKTSQIRGLYOGFSVS 180
DB 121 GAAGATSLCFYPPDLPARTRLADVGKSGTEREFGDCLVYKTSQIRGLYOGFSVS 180
OY 181 VGGIITTYRAAYGVYDPAKGLPDPKNTHTVYVSMIAQTVTAAGVSYPTVTRRRMM 240
DB 181 VGGIITTYRAAYGVYDPAKGLPDPKNTHTVYVSMIAQTVTAAGVSYPTVTRRRMM 240
OY 241 QSGRGADIMYTGVDCKWKIRFDEGKAFKFGAMSNVLRGNGAFVLYVDELKVI 298
DB 241 QSGRGADIMYTGVDCKWKIRFDEGKAFKFGAMSNVLRGNGAFVLYVDELKVI 298

RESULT 3
ADT2_HUMAN STANDARD: PRT; 298 AA.
ID ADT2_HUMAN P05141; O43350;
AC P05141; O43350;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Placenta;
RX MEDLINE=90375457; PubMed=2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wuzel J.;
RT "The human fibroblast adenine nucleotide translocator gene. Molecular
RT cloning and sequence."
RL J. Biol. Chem. 265:16060-16063(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Placenta;
RX MEDLINE=87166056; PubMed=3031073;
RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
RA Baserga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
RT growth-regulated."
RL J. Biol. Chem. 262:4355-4358(1987).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-Placenta;
RX Chen C.N., Su Y., Baybayan P., Sijuno A., Nagaraia R.,
RA Mazarelli R.A., Schlessinger D., Chen E.Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE-Placenta;
RX Becker M., Graves T., Ozerky P.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE-Liver;
RX MEDLINE=88124645; PubMed=2829183;
RA Houldsworth J., Atford G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC

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CC -----
DB EMBL: M57424; AAA51737.1; -
DB EMBL: J02683; AAA35579.1; -
DB EMBL: L78810; AAB39266.1; -
DB EMBL: AC004000; AAB96347.1; -
DB EMBL: J03591; AAA6749.1; -
DB PIR: A29132; A29132.
DB Genem: HGNC:10991; SLC25A5.
DB MIM: 300150; -
DB GO: GO:0005887; C: integral to plasma membrane; TAS.
DB GO: GO:0015207; F: adenine transporter activity; TAS.
DB GO: GO:0006832; P: small molecule transport; TAS.
DB InterPro: IPR002067; MLC carrier.
DB InterPro: IPR002030; MLC uncoupling.
DB InterPro: IPR001993; Mitoch. carrier.
DB Pfam: PF00153; Mito. carr. 3.
DB PRINTS: PR00926; MITOCARRIER.
DB PRINTS: PR00784; MTUNCOUPLING.
DB PROSITE: PS00215; MITOCH. CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12.. 29 1 (POTENTIAL).
FT TRANSMEM 73.. 91 2 (POTENTIAL).
FT TRANSMEM 117.. 134 3 (POTENTIAL).
FT TRANSMEM 176.. 195 4 (POTENTIAL).
FT TRANSMEM 214.. 231 5 (POTENTIAL).
FT TRANSMEM 273.. 291 6 (POTENTIAL).
FT REPEAT 1.. 111 1.
FT REPEAT 112.. 208 2.
FT REPEAT 209.. 298 3.
FT CONFLICT 6.. 6 V -> L (IN REF. 2).
FT CONFLICT 66.. 66 G -> E (IN REF. 2).
FT CONFLICT 111.. 111 R -> L (IN REF. 4 AND 5).
FT CONFLICT 162.. 162 V -> G (IN REF. 5).
SQ SEQUENCE 298 AA; 32895 MW; F973C3AED92C49D3 CRC64;

Query Match 94.8%; Score 1463; DB 1; Length 298;
Best Local Similarity 92.9%; Pred. No. 3; 8e-121;
Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

OY 1 MTEQAIISPAKDFLAGIAAISKTAIVAPIERVKLLIQVOHASKQIADKQYGIYDCIVR 60
DB 1 MTEQAVSFAPKDFLAGVAIAISKTAIVAPIERVKLLIQVOHASKQIADKQYGIYDCIVR 60
OY 61 IPKEGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAQNLASG 120
DB 61 IPKEGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAQNLASG 120
OY 121 GAAGATSLCFYPPDLPARTRLADVGKSGTEREFGDCLVYKTSQIRGLYOGFSVS 180
DB 121 GAAGATSLCFYPPDLPARTRLADVGKSGTEREFGDCLVYKTSQIRGLYOGFSVS 180
OY 181 VGGIITTYRAAYGVYDPAKGLPDPKNTHTVYVSMIAQTVTAAGVSYPTVTRRRMM 240
DB 181 VGGIITTYRAAYGVYDPAKGLPDPKNTHTVYVSMIAQTVTAAGVSYPTVTRRRMM 240
OY 241 QSGRGADIMYTGVDCKWKIRFDEGKAFKFGAMSNVLRGNGAFVLYVDELKVI 298
DB 241 QSGRGADIMYTGVDCKWKIRFDEGKAFKFGAMSNVLRGNGAFVLYVDELKVI 298

RESULT 4
ADT2_RAT STANDARD: PRT; 298 AA.
ID ADT2_RAT O09073;
AC O09073;
DT 01-FEB-1995 (Rel. 31, Created)

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DT 01-FEB-1995 (Rel. 31, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 GN (Adenine nucleotide translocator 2) (ANT 2).
 OS SLC25A5 OR ANT2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RX MEDLINE=94002161; PubMed=8399300;
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 encoding rat mitochondrial adenine nucleotide translocator.";
 RT Blochm. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
 CC SKELETAL MUSCLE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC -----
 DR EMBL: D12771; BAA02338.1; -
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; Mitoc_carri. 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER. 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32901 MW; 6A59204B987EF35 CRC64;
 Query Match 94.0%; Score 1451; DB 1; Length 298;
 Best Local Similarity 91.9%; Pred. No. 4.3e-120;
 Matches 272; Conservative 15; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTEBOAISPMKDFLAGGIAAISKTAAPITERYVLLIOVHASQIADROYKRTIVCIYR 60
 DB 1 MDAVASFMDPLAGVAAISTAVAPITERYVLLIOVHASQIADROYKRTIVCIYR 60
 QY 61 IPREGVLSFMRGNLANVIRYPTQALNFAKDKYKQIFLGVDKHTQEFWRYPAGNLAG 120
 DB 61 IPREGVLSFMRGNLANVIRYPTQALNFAKDKYKQIFLGVDKHTQEFWRYPAGNLAG 120
 QY 121 GAAGATSLCFVYPLDFARTRLAADVKSGETEREFGLDGCLVKTIRSDGIRGLYQGFVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLAADVKSGETEREFGLDGCLVKTIRSDGIRGLYQGFVS 180
 QY 181 VGGIITIRAAVFGVDTAGGMLPDKNTHTVVSMTIAQVTVANAGVSTPFDIVRRMM 240

DB 181 VGGIITIRAAVFGVDTAGGMLPDKNTHTVVSMTIAQVTVANAGVSTPFDIVRRMM 240
 QY 241 QSGRKGDIMWTGTVDYCDKRIFFDEGKAFFKAGANSVLRGMGAFVLYYDELK 296
 DB 241 QSGRKGDIMWTGTVDYCDKRIADDEGKAFFKAGANSVLRGMGAFVLYYDEIKR 296
 RESULT 5
 ADP2_MOUSE STANDARD; PRT; 298 AA.
 ID ADP2_MOUSE
 AC P51881; O61311; -
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, last sequence update)
 DT 28-FEB-2003 (Rel. 41, last annotation update)
 DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 DE (Adenine nucleotide translocator 2) (ANT 2).
 GN SLC25A5 OR ANT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX MEDLINE=97059403; PubMed=8903724;
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudautosomal genes and their mouse
 RT homologs.";
 RL Mamm. Genome 7:25-30(1996).
 RN [2]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA Sheldon J.G.;
 RL Thesis (1995), University of Cambridge, U.K.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RA Costel P., Laplace C.;
 RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP REVISIONS.
 RA Laplace C.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20432087; PubMed=10974536;
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide
 RT translocase 1 and 2 genes.";
 RL Gene 254:57-66(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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 CC -----
 CC EMBL: U27316; AAC52838.1; -
 CC EMBL: U10404; AAA19009.1; -
 CC EMBL: X70847; CAA50196.1; -
 CC EMBL: AF240003; AAF64471.1; -
 CC MGD: MGI:1353496; SLC25a5.
 DR InterPro: IPR002067; Mit_carrier.

DR InterPro: IPR002030; Mit_uncoupling.
 DR InterPro: IPR001993; Mitochond_carr. 3.
 DR Pfam: PF00153; mito_carr. 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER. 3.
 DR Mitochondion: Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32931 MM; 0798E04B987EFE20 CRC64;
 Query Match 93.6%; Score 1445; DB 1; Length 298;
 Best Local Similarity 91.6%; Pred. No. 1.4e-119;
 Matches 271; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTEQATSPADFLAGGIAAISTAVAPIERVKLLQVQHSKOIAADKOTKGIYDCIVR 60
 DB 1 MTDAAVSPADFLAGVAAIAISTAVAPIERVKLLQVQHSKOITADKQYGIIDCYVR 60
 QY 61 IPKQGVLSFWRGNLANVIRFPQALNFARFKDKYKQIFLGVDKHTQFMWYFAGNINL 120
 DB 61 IPKQGVLSFWRGNLANVIRFPQALNFARFKDKYKQIFLGVDKHTQFMWYFAGNINL 120
 QY 121 GAAGATSLCFYYPIDFARTRLAADVGKSGTEREFGGLDCLVKTSGINGLYOGFSVS 180
 DB 121 GAAGATSLCFYYPIDFARTRLAADVGKSGTEREFGGLDCLVKTSGINGLYOGFSVS 180
 QY 181 VGGIITRAAFGYVDTRAKGMLPDPKNTHTVSMIAQTVAVAGVSPDYVRRMM 240
 DB 181 VGGIITRAAFGYVDTRAKGMLPDPKNTHTVSMIAQTVAVAGVSPDYVRRMM 240
 QY 241 QSGRRGADIMYTGVDCKRKIFRDEGKAFKFGANSNVLKRGGAFLVLYDELKK 296
 DB 241 QSGRRGADIMYTGVDCKRKIFRDEGKAFKFGANSNVLKRGGAFLVLYDELKK 296

RESULT 6
 ADT1_RAT STANDARD; PRT; 298 AA.
 AC 005962;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
 DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
 GN SLC25A4 OR ANTI1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN: Sprague-Dawley, and Wistar; TISSUE: Heart, and Liver;
 RA MEDLINE: 94002161; PubMed: 8399300;
 RX Shinohara Y., Kamida M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 RT encoding rat mitochondrial adenine nucleotide translocator.",
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER
 CC EXTENT, IN BRAIN AND KIDNEY.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC -----
 DR EMBL: X61667; CAA43842.1; -;
 DR EMBL: D12770; BAA02237.1; -;
 DR PIR: I60173; I60173.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR InterPro: IPR001993; Mitochond_carr. 3.
 DR Pfam: PF00153; mito_carr. 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER. 3.
 DR Mitochondion: Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32989 MM; 66704FF78C6BC320 CRC64;
 Query Match 92.3%; Score 1424; DB 1; Length 298;
 Best Local Similarity 89.6%; Pred. No. 1e-117;
 Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQATSPADFLAGGIAAISTAVAPIERVKLLQVQHSKOIAADKOTKGIYDCIVR 60
 DB 1 MGDQALSLKPLFIAGGIAAISTAVAPIERVKLLQVQHSKOISAKQKGIIDCYVR 60
 QY 61 IPKQGVLSFWRGNLANVIRFPQALNFARFKDKYKQIFLGVDKHTQFMWYFAGNINL 120
 DB 61 IPKQGVLSFWRGNLANVIRFPQALNFARFKDKYKQIFLGVDKHTQFMWYFAGNINL 120
 QY 121 GAAGATSLCFYYPIDFARTRLAADVGKSGTEREFGGLDCLVKTSGINGLYOGFSVS 180
 DB 121 GAAGATSLCFYYPIDFARTRLAADVGKSGTEREFGGLDCLVKTSGINGLYOGFSVS 180
 QY 181 VGGIITRAAFGYVDTRAKGMLPDPKNTHTVSMIAQTVAVAGVSPDYVRRMM 240
 DB 181 VGGIITRAAFGYVDTRAKGMLPDPKNTHTVSMIAQTVAVAGVSPDYVRRMM 240
 QY 241 QSGRRGADIMYTGVDCKRKIFRDEGKAFKFGANSNVLKRGGAFLVLYDELKKV 298
 DB 241 QSGRRGADIMYTGVDCKRKIFRDEGKAFKFGANSNVLKRGGAFLVLYDELKKV 298

RESULT 7
 ADT1_MOUSE STANDARD; PRT; 298 AA.
 AC P48962; 062164;
 ID 01-FEB-1996 (Rel. 33, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
 DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (MANC1).
 GN SLC25A4 OR ANTI1 OR ANCI1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6; TISSUE=Brain;
 RX MEDLINE=97059403; PubMed=8903724;
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudautosomal genes and their mouse
 RL homologs".
 RN Mamm. Genome 7:25-30(1996).
 [2]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c; TISSUE=Muscle;
 RA Laplace C., Costet P.;
 RT Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN RP SEQUENCE FROM N.A.
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide
 RL translocase 1 and 2 genes."
 RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [4]
 RN RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.D., Fellngold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.L., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheiner C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci R., Prange C.,
 RA Rata S.S., Loeuallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Roark S.A., McKernan P.J., McKernan K.T., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heltan E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gilwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

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 CC or send an email to license@sib.ch).

 DR EMBL; U27315; AAC52837.1; -;
 DR EMBL; X74510; CAA52616.1; -;
 DR EMBL; AF240002; AAF64470.1; -;
 DR EMBL; BC003791; AAH03791.1; -;
 DR EMBL; BC026925; AAH26925.1; -;
 DR PIR; S37210; S37210
 DR MGD; MGI:1353495; Slc25a4.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PRO0926; MITOCARRIER.
 DR PRINTS; PRO0784; MTNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.

KV	Multicene family; Inner membrane; Repeat; Transmembrane; Transport;
RN	TRANSMEM 12 29 1 (POTENTIAL).
FT	TRANSMEM 73 91 2 (POTENTIAL).
FT	TRANSMEM 117 134 3 (POTENTIAL).
FT	TRANSMEM 176 195 4 (POTENTIAL).
FT	TRANSMEM 231 291 5 (POTENTIAL).
FT	TRANSMEM 273 291 6 (POTENTIAL).
FT	REPEAT 1 110 1.
FT	REPEAT 111 208 2.
FT	REPEAT 209 298 3.
FT	CONFLICT 136 136 F -> L (IN REF. 1).
SQ	SEQUENCE 298 AA; 32904 MW; 3A849FEAB0981462 CRC64;
Query Match	91.9%; Score 1418; DB 1; Length 298;
Blast Local Similarity	88.9%; Pred. No. 3.4e-117;
Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps	
OY	1 MTEGALISFANDFLAGGIAMAIKSTVAAPIERVELLLQVOHASKOIMADKOYGIVDCIWR 60
DB	1 MGDDAFSLFDLDELGLGGIAAAVSRTAVAPIERVKLLLOVHASKOISAERKGIIIDCYVR 60
OY	61 IPKKOGLSFWRGNAVIRYPPTQALNFPAFKKYKOIFLGVDKRTOFMRFACGLASG 12
DB	61 IPKOGLSFWRGNLANVIRFPQALNFAFKKYKOIFLGVDKRKFMRPFAGLASG 12
OY	121 GAAGATSLCEFYPLDFEARTRLAADVGKSCTEREFGSLDCLVIKITSDSIRGLYGSFSYS 18
DB	121 GAAGATSLCEFYPLDFEARTRLAADVGKSSQREFNGLDOLTRIEPSDLKGLGYGSFSYS 18
OY	181 VQGIIITRAAYFCGYTPDAKGMTLDPDKRTHILVYSWMTAQVTAVAGYSTPEPTVRRMM 24
DB	181 VOGLIIITRAAYFCGYTPDAKGMTLPDPKNVHLIVSWMAIGSTAATAAGLVSPFTVRRMM 24
OY	241 QSGRKGAIDMYTGTGDCKRIKFRDECGKAFFKSAWSNVLRMGCAFLVLVDLKKVI 298
DB	241 QSGRKGAIDMYTGTGLDCKRIADEGMNAEFKRSANSYLKMGCAFVLVLVDLIKVI 298

RESULT 8
ADTL_BOVIN STANDARD; PRT; 297 AA.
AC P02722;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP carrier protein, heart isoform T1 (ADP/ATP translocase 1)
DE (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=69229093; PubMed=2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial Adp/Atp translocase expressed differences in various tissues";
RL Biochemistry 28:866-873(1989).
[2]
RP SEQUENCE.
RX MEDLINE=82188267; PubMed=7076130;
RA Aquila H., Mistra D., Eulitz M., Klingenberg M.;
RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondria.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).
[3]
RP SEQUENCE OF 207-297 FROM N.A.
RX MEDLINE=66295775; PubMed=3017341;
RA "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and

```

RT an unusually short 3'-noncoding sequence."
RL Blochem. Biophys. Res. Commun. 138:850-857(1986).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
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CC -----
DR EMBL, M13783; AAA30363.1; -.
DR EMBL, M24102; AAA30768.1; -.
DR PIR, A43646; XMO.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR002030; Mlt_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mltc_carri; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
DR Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family; Methylation.
FT INIT_MET 0
FT MOD_RES 1 1 BLOCKED.
FT MOD_RES 51 51 METHYLATION (POTENTIAL).
FT TRANSMEM 11 28 1 (POTENTIAL).
FT TRANSMEM 72 90 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 175 194 4 (POTENTIAL).
FT TRANSMEM 213 230 4 (POTENTIAL).
FT TRANSMEM 272 290 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 207 2.
FT REPEAT 208 297 3.
SQ SEQUENCE 297 AA; 32836 MW; A582D3C4A40AEB48 CRC64;

Query Match 91.8%; Score 1417; DB 1; Length 297;
Best Local Similarity 89.2%; Pred. No. 4,1e-117;
Matches 265; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

2 TEQAISPAKDFLAGIAAIAISTAVAPIERVKLLQVOHASKOIAADKQYKIVDCIYRI 61
1 SPOALSFKDFLAGGVAIAISTAVAPIERVKLLQVOHASKOIAENKQYKIIQCVARI 60
62 PREQGVLSFWNGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHKQFRRYRAGNLSGG 121
61 PREQGVLSFWNGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHKQFRRYRAGNLSGG 120
122 AAGATSLCFVYPLDFARTRIADVAGKSGTEREFGDCLVITKSDGIRGLYOGFSYV 181
121 AAGATSLCFVYPLDFARTRIADVAGKSGTEREFGDCLVITKSDGIRGLYOGFSYV 180
182 OGIIIRYRAAYEGVYDTAKGMLPDPKNTHTVSWMTAQVTAVAGVSYPTDTRRRMMQ 241
181 OGIIIRYRAAYEGVYDTAKGMLPDPKNTHTVSWMTAQVTAVAGVSYPTDTRRRMMQ 240
242 SGRKADIMYGTGTCWKRIRFDEGGKAFKFGKAMSNVLRGNGCAFLVLYDXLAKYI 298
241 SGRKADIMYGTGTCWKRIRFDEGGKAFKFGKAMSNVLRGNGCAFLVLYDXLAKYI 297

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DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
DE translocase 1) (Adenine nucleotide translocator 1) (ANT1).
GN SLC25A4 OR ANT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89236396; PubMed=2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
RT ADP/ATP translocase."
RL J. Mol. Biol. 206:261-280(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89340499; PubMed=2547778;
RA Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,
RA Fukuyama R., Maekawa M., Shimizu Y., Shintzu N., Wallace D.C.;
RT "A human muscle adenine nucleotide translocator gene has four exons,
RT is located on chromosome 4, and is differentially expressed."
RL J. Biol. Chem. 264:13998-14004(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88041149; PubMed=2823266;
RA Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;
RT "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack
RT of a leader peptide, divergence from a fibroblast translocator cDNA,
RT and coevolution with mitochondrial DNA genes."
RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Fellngold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buertow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosch S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 1-37 FROM N.A.
RX TISSUE=Liver;
RC MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Altardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
RN [6]
RP VARIANTS PEO PRO-114 AND MET-289.
RX MEDLINE=20385067; PubMed=10926541;
RA Kaukonen J., Juselius J.K., Tiranli V., Kytala A., Zeviani M.,
RA Comi G.P., Keranen J., Peltonen L., Skomlainen A.;
RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance."
RL Science 289:782-785(2000).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE

```


FT TRANSMEM 178 197 4 (POTENTIAL).
 FT TRANSMEM 216 233 5 (POTENTIAL).
 FT TRANSMEM 275 293 6 (POTENTIAL).
 SQ SEQUENCE 301 AA; 32863 MW; 4CC9E17C9F8DA08B CRC64;

Query Match 78.0%; Score 1204; DB 1; Length 301;
 Best Local Similarity 77.7%; Pred. No. 2,1e-98;
 Matches 233; Conservative 23; Mismatches 42; Indels 2; Gaps 1;

QY. 1 MTEQA--ISPAKDELAGIAAIAIKTAAPLIERKLLQYOHASKOIADK--QYKIVDCIPIPK 58
 1 MTKRADYGFRAKDLAGISAAVSKTAVPIERKLLQYOHASKOIADKQYKIVDCI 60
 Db 119 SGGAGATSLCFVYPLDFAFRTLAADVGSKSTEREFRGLDCLVKIKRSGIRGLYGSF 178
 121 SGGAGATSLCFVYPLDFAFRTLAADVGSKSTEREFRGLDCLVKIKRSGIRGLYGSF 180
 QY 179 VSVGGITTYRAAYFGVYDTAKGMLDPKNTIIVSMIAQTVAAGVSYEPDVTARRM 238
 181 VSVGGITTYRAAYFGVYDTAKGMLDPKNTIIVSMIAQTVAAGVSYEPDVTARRM 240
 Db 239 MMSGRKADIMTYGVDCRKRIFRDEGKAFFEGANSNVLKRGAGFVLVDELKVI 298
 241 MMSGRKADIMTYGVDCRKRIFRDEGKAFFEGANSNVLKRGAGFVLVDELKVI 300

RESULT 12
 ADT_CHLKE STANDARD; PRT; 339 AA.

AC P31692;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
 translocator) (ANT).
 OS Chlorocella kessleri.
 OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
 OC Chlorellaceae; Chlorocella.
 NC NCBL_TaxID=3074;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92084708; Pubmed=1748677;
 RA Hlgarth C., Sauer N., Tanner W.;
 RT "Glucose increases the expression of the ATP/ADP translocator and the
 RT glyceraldehyde-3-phosphate dehydrogenase genes in Chlorocella.";
 RL J. Biol. Chem. 266:24044-24047(1991).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC
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 CC
 CC EMBL: M76669; AAA33027.1; -
 DR PIR: A41677; A41677.
 DR InterPro: IPR002067; Mtc_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mtc_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.

KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 45 62 1 (POTENTIAL).
 FT TRANSMEM 108 126 2 (POTENTIAL).
 FT TRANSMEM 151 168 3 (POTENTIAL).
 FT TRANSMEM 209 228 4 (POTENTIAL).
 FT TRANSMEM 248 265 5 (POTENTIAL).
 FT TRANSMEM 304 322 6 (POTENTIAL).
 SQ SEQUENCE 339 AA; 36686 MW; 54779734A3B3942 CRC64;

Query Match 63.4%; Score 978; DB 1; Length 339;
 Best Local Similarity 66.9%; Pred. No. 1.6e-78;
 Matches 198; Conservative 26; Mismatches 64; Indels 8; Gaps 5;

QY 6 ISPAKDELAGIAAIAIKTAAPLIERKLLQYOHASKOIADK--QYKIVDCIPIPK 63
 39 MAFFKDLIAGTAGAISAKTAVPIERKLLQYOHASKOIADKQYKIVDCIPIPK 98
 Db 64 ECGVLSWRKRNLANVITFFPQALNFAFKKQKQIFLGVDKHTQFWRITAGNLASGGA 123
 99 ECGVLSWRKRNLANVITFFPQALNFAFKKQKQIFLGVDKHTQFWRITAGNLASGGA 157
 QY 124 GATSLCFVYPLDFAFRTLAADVGSKSTEREFRGLDCLVKIKRSGIRGLYGSFVSVOG 183
 158 GAGSLLVYPLDFAFRTLAADVGSKSTEREFRGLDCLVKIKRSGIRGLYGSFVSVOG 216
 Db 184 IITTYRAAYFGVYDTAKGMLDPKNTIIVSMIAQTVAAGVSYEPDVTARRM 242
 217 IITTYRAAYFGVYDTAKGMLDPKNTIIVSMIAQTVAAGVSYEPDVTARRM 276
 QY 243 GRKADIMTYGVDCRKRIFRDEGKAFFEGANSNVLKRGAGFVLVDELKVI 298
 277 GRKADIMTYGVDCRKRIFRDEGKAFFEGANSNVLKRGAGFVLVDELKVI 329

RESULT 13
 ADT_YEAST STANDARD; PRT; 307 AA.

AC P18236;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE ADP/ATP carrier protein 3 (ADP/ATP translocase 3) (Adenine nucleotide
 translocator 3) (ANT 3).
 DE AAC3 OR YBR085W OR YBR0753.
 GN AAC3 OR YBR085W OR YBR0753.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 NC NCBL_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90324269; Pubmed=2165073;
 RA Kolarov J., Kolarova N., Nelson N.;
 RT "A third ADP/ATP translocator gene in yeast.";
 RL J. Biol. Chem. 265:12711-12716(1990).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN=S288C;
 CC STRAIN=S288C;
 CC STRAIN=S288C;
 RA Feldmann H., Mannhaupt G., Schwarzlose C., Vetter I.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC

GN ANCI OR SPBC530.10C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=96257204; PubMed=8675018;
 RT Couzin N., Trezeguet V., Saux A.L., Lauguin G.J.M.;
 RT "Cloning of the gene encoding the mitochondrial adenine nucleotide
 RT carrier of Schizosaccharomyces pombe by functional complementation in
 RT Saccharomyces cerevisiae.";
 RL Gene 171:113-117(1996).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Soutos J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
 RA Jones K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeli C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Voiclaert G., Aert R., Rodden J., Gymnopoulos B.,
 RA Welfens I., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Filtz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Leleure V., Mottier S.,
 RA Gallibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RA "The genome sequence of Schizosaccharomyces pombe.";
 RA Nature 415:871-880(2002).
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC -----
 CC EMBL: Z49974; CAA90275.1; -;
 CC EMBL: AL023634; CAA19176.1; -;
 CC FIR: T40526; T40526.
 CC GeneDB_Spomb: SPBC530.10C; -;
 CC InterPro: IPR002067; Mit_carrier.
 CC InterPro: IPR001993; Mitoch_carrier.
 CC Pfam: PF00153; mito_carr_3.
 CC PRINTS: PR00926; MITOCARRIER.
 CC PROSITE: PS00215; MITOCH_CARRIER; 2.
 CC Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 28 48 1 (POTENTIAL).
 FT TRANSMEM 93 111 2 (POTENTIAL).

FT TRANSMEM 131 151 3 (POTENTIAL).
 FT TRANSMEM 197 217 4 (POTENTIAL).
 FT TRANSMEM 222 242 5 (POTENTIAL).
 FT TRANSMEM 289 309 6 (POTENTIAL).
 SQ SEQUENCE 322 AA; 35020 MW; 8AC3D16A40F41AFC CRC64;
 Query Match 49.8%; Score 769; DB 1; Length 322;
 Best Local Similarity 53.6%; Pred. No. 3.3e-60;
 Matches 158; Conservative 50; Mismatches 75; Indels 12; Gaps 6;
 QY 7 SFAKDLGGIAAIAIKTAVAPIERVKLLIOVHASKQIAADK---QYGIYDCIRIP 63
 DB 26 TFFPDMGGSAAVSTAAPIERVKLLIQND--DMTRAGLSHRHVGIGCFRRTPA 83
 QY 64 EDCVLSFWRGNLANVRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASGAA 123
 DB 84 EEGVISLWRGNTANVLRYPPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASGAA 142
 QY 124 GATSLCFVYPLDPAFRRLAADV--GKSGTEREERGLDCLVTKSDGIRGLYQGFVSIV 181
 DB 143 GAASLFFVYSLDPAFRRLANDAKSARKGGERQFNGLVYRKYRSDGLRGLYRGFSPV 202
 QY 182 OGIIYRAAYEGVYDPAKG--MLDPKNTHTVYSMTAQTVTANAGVYSYEDFVRRRMM 240
 DB 203 VGIIVYRGILFGMDITLKPVLVGLPGLGNFLASFLIGMAVTGSGVASTPLDIRRRMM 262
 QY 241 QSGRKADIVYTVTCWKRIFRDEGKAFKFGAMSNTVLRMGAVLVLYDELK 295
 DB 263 TSGEA---VYSSSFEQGRQIILKEGARSFKAGNINLRGVAGAVLSTYDQV 314

Search completed: August 28, 2003, 19:39:32
 Job time : 13.0134 secs

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: August 28, 2003, 19:34:36 ; Search time 50.3897 Seconds
(without alignments)
1526.099 Million cell updates/sec

Title: US-09-811-132-33

Perfect score: 1543
Sequence: 1 MTEQAISFADFLAGIAA.....LRGKGAFVLVYDELKKVI 298

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 segs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MNC:*
8: SP_ORNITHINE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1474	95.5	298	13	OBAYM3
2	1451	94.0	298	6	OB8QH5
3	1446	93.7	298	13	OB8H10
4	1422	92.2	298	6	OB6373
5	1421	92.1	298	13	OB91M9
6	1414	91.6	298	11	OB8V19
7	1409	91.3	298	13	OB8PR1
8	1406	91.1	298	13	OB8PR2
9	1402	90.9	298	13	OB8PR3
10	1300	84.3	299	5	O95VX4
11	1259	81.6	317	13	O91336
12	1254.5	81.3	312	5	OB8RA0
13	1235.5	80.1	300	5	OB8HMS
14	1187.5	77.0	288	5	O44093
15	1183.5	76.7	288	5	O44094
16	1176.5	76.2	304	5	O25129

17	1159	75.1	254	11	OB8K05	OB8K05 mus musculus
18	1137.5	73.7	307	5	O62526	O62526 drosophila
19	1119	72.5	315	4	O9H0C2	O9H0C2 homo sapien
20	1041	67.5	313	5	O21103	O21103 caenorhabd
21	1039	67.3	313	5	P91410	P91410 caenorhabd
22	1038	67.3	300	5	O45865	O45865 caenorhabd
23	1036.5	67.2	310	10	OB8727	OB8727 phytothor
24	996	64.5	309	5	O97470	O97470 dictyostell
25	993.5	64.4	300	5	O01813	O01813 caenorhabd
26	993	64.4	300	5	O17407	O17407 caenorhabd
27	973.5	63.1	318	5	O9B136	O9B136 toxoplasma
28	947	61.4	301	5	OB8J34	OB8J34 plasmodium
29	946.5	61.3	307	8	O9XM22	O9XM22 ascaris suu
30	944	61.2	301	5	O25692	O25692 plasmodium
31	944	61.2	301	5	OB8VR4	OB8VR4 euplores sp
32	943	61.1	301	5	O26006	O26006 plasmodium
33	936	60.7	305	5	OB8VR7	OB8VR7 nyctotherus
34	932	60.4	308	5	OB8VR8	OB8VR8 nyctotherus
35	924	59.9	306	5	OB8VR5	OB8VR5 nyctotherus
36	924	59.9	308	5	O9XS69	O9XS69 sus scrofa
37	827	53.6	170	6	O9X8M1	O9X8M1 yarrowia
38	778.5	50.5	305	3	OB8J0M2	OB8J0M2 yarrowia
39	767.5	49.7	302	3	P91270	P91270 caenorhabd
40	764	49.5	326	5	O76286	O76286 trypanosoma
41	760	49.3	307	5	O74260	O74260 candida par
42	759	49.2	303	3	O18683	O18683 caenorhabd
43	756.5	48.8	306	5	O26697	O26697 trypanosoma
44	753	48.8	307	5	OB8J0U1	OB8J0U1 gaemannomy
45	749	48.5	315	3		

ALIGNMENTS

RESULT 1
ID OBAYM3 PRELIMINARY; PRT; 298 AA.
AC OBAYM3;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ATP/ADP antiporter.
OS AVANT.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba Y.;
RT "Cold-induced mitochondrial uncoupling and expression of chicken UCP
and ANT mRNA in chicken skeletal muscle.";
RL FEBS Lett. 0:0-0(2002).
DR EMBL; AB088686; BAC15533.1;
SQ SEQUENCE 298 AA; 32847 MW; 1174C5E400A10D CRC64;

Query Match 95.5%; Score 1474; DB 13; Length 298;
Best local Similarity 93.0%; Pred. No. 2.5e-125;
Matches 277; Conservative 14; Mismatches 7; Indels 0; Gaps 0;
OY 1 MTEQAISFADFLAGIAAISKTAIVAPIERVKLLLOVHASKQTAADROYGIYDCIYR 60
DB 1 MADQAIKFLDKLAKGVAAAIKTAIVAPIERVKLLLOVHASKQTAADROYGIYDCIYR 60
OY 61 IRKEQVLSFWRGNTANVIRFPTQALNFAFDKTKQIFLAGVDKHTQFWRFPAGNLASG 120
DB 61 IRKEQVLSFWRGNTANVIRFPTQALNFAFDKTKQIFLAGVDKHTQFWRFPAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTRLAADVGKSTEEFEGKGLGCLYKTKSDGIRGLYQGFVS 180
DB 121 GAAGATSLCFVYPLDFARTRLAADVGKADREDFSGIDGLVTKIKSDGLRGLYQGFVS 180

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QY 181 VGGIIRAAVFGVYDTAGKMLDPKNTHTIVSMMIAQVTAVAGVSPEDTVRRMM 240
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 VGGIIRAAVFGIYDTAGKMLDPKNTHTIVSMMIAQVTAVAGVSPEDTVRRMM 240
QY 241 QSGRKADIMYTGTVCKRKIFDEGKAFKAGMSNVLRGKAGAVLVLYDELKVI 298
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 QSGRKADIMYSGTIDCKWKRIADGKAFKAGMSNVLRGKAGAVLVLYDEKVI 298

RESULT 2
OSQHS PRELIMINARY; PRT; 298 AA.
ID OSQHS
AC OSQHS;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Adenine nucleotide translocator 2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamazaki N., Shinohara Y., Tanida K., Terada H.;
RT "Structural properties of mammalian mitochondrial ADP/ATP carriers:
RT identification of possible amino acids that determine functional
RT differences in its isoforms.";
RL Mitochondrion 1:371-379(2002).
DR EMBL; AB065433; BAB84673.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carri; 3.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
SQ SEQUENCE 298 AA; 32955 MW; CB6897BB987B79C0 CRC64;

Query Match 94.0%; Score 1451; DB 6; Length 298;
Best Local Similarity 92.2%; Pred. No. 3e-123;
Matches 273; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAISTKVAAPIERVKLLQVGHASKQIADKQKGIYDCIVR 60
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MTEAAVSFAKDFLAGGIAAISTKVAAPIERVKLLQVGHASKQIADKQKGIYDCIVR 60
QY 61 IPEQGVLSFWKRNLANVIRYPTQALNFAFKYKQIFLGVDKTKQFWRRFAGNLASG 120
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 IPEQGVLSFWKRNLANVIRYPTQALNFAFKYKQIFLGVDKTKQFWRRFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFAKRLADVGKSGTEREFGIGDCLVITKTSKGIXQGSYS 180
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GAAGATSLCFVYPLDFAKRLADVGKSGTEREFGIGDCLVITKTSKGIXQGSYS 180
QY 181 VGGIIRAAVFGVYDTAGKMLDPKNTHTIVSMMIAQVTAVAGVSPEDTVRRMM 240
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 VGGIIRAAVFGIYDTAGKMLDPKNTHTIVSMMIAQVTAVAGVSPEDTVRRMM 240
QY 241 QSGRKADIMYTGTVCKRKIFDEGKAFKAGMSNVLRGKAGAVLVLYDELKVI 296
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 QSGRKADIMYSGTIDCKWKRIADGKAFKAGMSNVLRGKAGAVLVLYDEIKK 296

RESULT 3
OSQHS PRELIMINARY; PRT; 298 AA.
ID OSQHS
AC OSQHS;
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Solute carrier family 25 member 5 protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.

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OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2035902; PubMed=12006978;
RA Gollig G., Amsterdam A., Sun Z., Antonelli M., Maldonado E., Chen W.,
RA Burgess S., Haidl M., Artzt K., Farrington S., Lin S.-T., Nissen R.M.,
RA Hopkins N.;
RT "Insertional mutagenesis in zebrafish rapidly identifies genes
RT essential for early vertebrate development.";
RL Nat. Genet. 31:135-140(2002).
DR EMBL; AF506216; AAM34660.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR Pfam; PF00153; mito_carri; 3.
DR PRINTS; PR00784; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
SQ SEQUENCE 298 AA; 32763 MW; D78663CF65C5D39 CRC64;

Query Match 93.7%; Score 1446; DB 13; Length 298;
Best Local Similarity 91.9%; Pred. No. 8.5e-123;
Matches 274; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAISTKVAAPIERVKLLQVGHASKQIADKQKGIYDCIVR 60
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MTEAISFAKDFLAGGIAAISTKVAAPIERVKLLQVGHASKQIADKQKGIYDCIVR 60
QY 61 IPEQGVLSFWKRNLANVIRYPTQALNFAFKYKQIFLGVDKTKQFWRRFAGNLASG 120
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 IPEQGVLSFWKRNLANVIRYPTQALNFAFKYKQIFLGVDKTKQFWRRFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFAKRLADVGKSGTEREFGIGDCLVITKTSKGIXQGSYS 180
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GAAGATSLCFVYPLDFAKRLADVGKSGTEREFGIGDCLVITKTSKGIXQGSYS 180
QY 181 VGGIIRAAVFGVYDTAGKMLDPKNTHTIVSMMIAQVTAVAGVSPEDTVRRMM 240
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 VGGIIRAAVFGIYDTAGKMLDPKNTHTIVSMMIAQVTAVAGVSPEDTVRRMM 240
QY 241 QSGRKADIMYTGTVCKRKIFDEGKAFKAGMSNVLRGKAGAVLVLYDELKVI 298
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 QSGRKADIMYSGTIDCKWKRIADGKAFKAGMSNVLRGKAGAVLVLYDELKVI 298

RESULT 4
OSQHS PRELIMINARY; PRT; 298 AA.
ID OSQHS
AC OSQHS;
DT 01-JUN-1998 (TEMBLrel. 06, Created)
DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue-Skeletal muscle;
RA Yamaguchi N., Kasai M.;
RT "Identification of a 30kDa calsequestrin-binding protein, which
RT regulates calcium release from sarcoplasmic reticulum of rabbit
RT skeletal muscle.";
RL J. Biochem. 335:541-547(1998).
DE -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB009386; BA423777.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR Pfam; PF00153; mito_carri; 3.
DR PRINTS; PR00784; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.

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NCBI_TaxID=8410;

OX [1] SEQUENCE FROM N.A.
 RA MEDLINE=99083429; PubMed=9866197;
 RA Mura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromorphic sex chromosomes
 of a sex-linked gene, ADP/ATP translocase.";
 RT Z, W, X, and Y in the frog *Rana rugosa*, inferred from the sequences of
 RT a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AB008453; BAA36513.1; -;
 DR EMBL; AB008456; BAA36506.1; -;
 DR EMBL; AB008461; BAA36511.1; -;
 DR EMBL; AB008462; BAA36512.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR002030; Mlt_uncoupling.
 DR Pfam: PF00153; mltocarr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Membrane; Transmembrane; Transport.
 KW SEQUENCE 298 AA; 33054 MW; BOE23AD56F548D36 CRC64;

Query Match 91.3%; Score 1409; DB 13; Length 298;
 Best Local Similarity 86.6%; Pred. No. 1.9e-119;
 Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

OY 1 MTEQAISFADFAGLGGIAAISTKAVAPIERVKLLLOVHASKQIADKQYKGIQVDCIVR 60
 1 MTDAISFADFAGLGGIAAISTKAVAPIERVKLLLOVHASKQITADKQYKGIQVDCIVR 60
 DB 181 VGGIIIRAAVFGYIDTAKGMLPDKNTHTVSMIAQTYAVAGVSYFEDYRRMM 240
 181 VGGIIIRAAVFGYIDTAKGMLPDKNTHTVSMIAQTYAVAGVSYFEDYRRMM 240
 OY 61 IPKQGVLSFWRGMLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 61 IPKQGVLSFWRGMLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 DB 61 IPKQGVLSFWRGMLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 61 IPKQGVLSFWRGMLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 OY 121 GAAGATSLCFYPLDFARTRLAADVSGSGTEREREGIDGLVTKTSDGIRGLYOGFSVS 180
 121 GAAGATSLCFYPLDFARTRLAADVSGSGTEREREGIDGLVTKTSDGIRGLYOGFSVS 180
 DB 121 GAAGATSLCFYPLDFARTRLAADVSGSGTEREREGIDGLVTKTSDGIRGLYOGFSVS 180
 121 GAAGATSLCFYPLDFARTRLAADVSGSGTEREREGIDGLVTKTSDGIRGLYOGFSVS 180
 OY 181 VGGIIIRAAVFGYIDTAKGMLPDKNTHTVSMIAQTYAVAGVSYFEDYRRMM 240
 181 VGGIIIRAAVFGYIDTAKGMLPDKNTHTVSMIAQTYAVAGVSYFEDYRRMM 240
 DB 181 VGGIIIRAAVFGYIDTAKGMLPDKNTHTVSMIAQTYAVAGVSYFEDYRRMM 240
 181 VGGIIIRAAVFGYIDTAKGMLPDKNTHTVSMIAQTYAVAGVSYFEDYRRMM 240
 OY 241 QSGRKADIMTGTGVCDCWKRTIFRDEGKAFKFGKMSVNLKMGAFVLVYLDELKYYI 298
 241 QSGRKADIMTGTGVCDCWKRTIFRDEGKAFKFGKMSVNLKMGAFVLVYLDELKYYI 298
 DB 241 QSGRKADIMTGTGVCDCWKRTIFRDEGKAFKFGKMSVNLKMGAFVLVYLDELKYYI 298
 241 QSGRKADIMTGTGVCDCWKRTIFRDEGKAFKFGKMSVNLKMGAFVLVYLDELKYYI 298

RESULT 8

OYPRH2 PRELIMINARY; PRT; 298 AA.

AC OYPRH2;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS *Rana rugosa* (Winkled frog).
 OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99083429; PubMed=9866197;
 RA Mura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromorphic sex chromosomes
 of a sex-linked gene, ADP/ATP translocase.";
 RT Z, W, X, and Y in the frog *Rana rugosa*, inferred from the sequences of
 RT a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AB008453; BAA36510.1; -;
 DR EMBL; AB008458; BAA36508.1; -;
 DR EMBL; AB008459; BAA36509.1; -;

InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR002030; Mlt_uncoupling.
 DR Pfam: PF00153; mltocarr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Membrane; Transmembrane; Transport.
 KW SEQUENCE 298 AA; 33082 MW; BOE225E867599A06 CRC64;

Query Match 91.1%; Score 1406; DB 13; Length 298;
 Best Local Similarity 86.3%; Pred. No. 3.6e-119;
 Matches 263; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

OY 1 MTEQAISFADFAGLGGIAAISTKAVAPIERVKLLLOVHASKQIADKQYKGIQVDCIVR 60
 1 MTDAISFADFAGLGGIAAISTKAVAPIERVKLLLOVHASKQITADKQYKGIQVDCIVR 60
 DB 181 VGGIIIRAAVFGYIDTAKGMLPDKNTHTVSMIAQTYAVAGVSYFEDYRRMM 240
 181 VGGIIIRAAVFGYIDTAKGMLPDKNTHTVSMIAQTYAVAGVSYFEDYRRMM 240
 OY 61 IPKQGVLSFWRGMLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 61 IPKQGVLSFWRGMLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 DB 61 IPKQGVLSFWRGMLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 61 IPKQGVLSFWRGMLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 OY 121 GAAGATSLCFYPLDFARTRLAADVSGSGTEREREGIDGLVTKTSDGIRGLYOGFSVS 180
 121 GAAGATSLCFYPLDFARTRLAADVSGSGTEREREGIDGLVTKTSDGIRGLYOGFSVS 180
 DB 121 GAAGATSLCFYPLDFARTRLAADVSGSGTEREREGIDGLVTKTSDGIRGLYOGFSVS 180
 121 GAAGATSLCFYPLDFARTRLAADVSGSGTEREREGIDGLVTKTSDGIRGLYOGFSVS 180
 OY 181 VGGIIIRAAVFGYIDTAKGMLPDKNTHTVSMIAQTYAVAGVSYFEDYRRMM 240
 181 VGGIIIRAAVFGYIDTAKGMLPDKNTHTVSMIAQTYAVAGVSYFEDYRRMM 240
 DB 181 VGGIIIRAAVFGYIDTAKGMLPDKNTHTVSMIAQTYAVAGVSYFEDYRRMM 240
 181 VGGIIIRAAVFGYIDTAKGMLPDKNTHTVSMIAQTYAVAGVSYFEDYRRMM 240
 OY 241 QSGRKADIMTGTGVCDCWKRTIFRDEGKAFKFGKMSVNLKMGAFVLVYLDELKYYI 298
 241 QSGRKADIMTGTGVCDCWKRTIFRDEGKAFKFGKMSVNLKMGAFVLVYLDELKYYI 298
 DB 241 QSGRKADIMTGTGVCDCWKRTIFRDEGKAFKFGKMSVNLKMGAFVLVYLDELKYYI 298
 241 QSGRKADIMTGTGVCDCWKRTIFRDEGKAFKFGKMSVNLKMGAFVLVYLDELKYYI 298

RESULT 9

OYITC4 PRELIMINARY; PRT; 298 AA.

AC OYITC4;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS *Rana rugosa* (Winkled frog).
 OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99083429; PubMed=9866197;
 RA Mura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromorphic sex chromosomes
 of a sex-linked gene, ADP/ATP translocase.";
 RT Z, W, X, and Y in the frog *Rana rugosa*, inferred from the sequences of
 RT a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AB008457; BAA36507.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR002030; Mlt_uncoupling.
 DR Pfam: PF00153; mltocarr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Membrane; Transmembrane; Transport.
 KW SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;

Query Match 90.9%; Score 1402; DB 13; Length 298;
 Best Local Similarity 87.9%; Pred. No. 8.3e-119;
 Matches 262; Conservative 21; Mismatches 15; Indels 0; Gaps 0;

OY 1 MTEQAISFADFAGLGGIAAISTKAVAPIERVKLLLOVHASKQIADKQYKGIQVDCIVR 60
 1 MTDAISFADFAGLGGIAAISTKAVAPIERVKLLLOVHASKQITADKQYKGIQVDCIVR 60
 DB 181 VGGIIIRAAVFGYIDTAKGMLPDKNTHTVSMIAQTYAVAGVSYFEDYRRMM 240
 181 VGGIIIRAAVFGYIDTAKGMLPDKNTHTVSMIAQTYAVAGVSYFEDYRRMM 240
 OY 61 IPKQGVLSFWRGMLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 61 IPKQGVLSFWRGMLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 DB 61 IPKQGVLSFWRGMLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 61 IPKQGVLSFWRGMLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 OY 121 GAAGATSLCFYPLDFARTRLAADVSGSGTEREREGIDGLVTKTSDGIRGLYOGFSVS 180
 121 GAAGATSLCFYPLDFARTRLAADVSGSGTEREREGIDGLVTKTSDGIRGLYOGFSVS 180
 DB 121 GAAGATSLCFYPLDFARTRLAADVSGSGTEREREGIDGLVTKTSDGIRGLYOGFSVS 180
 121 GAAGATSLCFYPLDFARTRLAADVSGSGTEREREGIDGLVTKTSDGIRGLYOGFSVS 180
 OY 181 VGGIIIRAAVFGYIDTAKGMLPDKNTHTVSMIAQTYAVAGVSYFEDYRRMM 240
 181 VGGIIIRAAVFGYIDTAKGMLPDKNTHTVSMIAQTYAVAGVSYFEDYRRMM 240
 DB 181 VGGIIIRAAVFGYIDTAKGMLPDKNTHTVSMIAQTYAVAGVSYFEDYRRMM 240
 181 VGGIIIRAAVFGYIDTAKGMLPDKNTHTVSMIAQTYAVAGVSYFEDYRRMM 240
 OY 241 QSGRKADIMTGTGVCDCWKRTIFRDEGKAFKFGKMSVNLKMGAFVLVYLDELKYYI 298
 241 QSGRKADIMTGTGVCDCWKRTIFRDEGKAFKFGKMSVNLKMGAFVLVYLDELKYYI 298
 DB 241 QSGRKADIMTGTGVCDCWKRTIFRDEGKAFKFGKMSVNLKMGAFVLVYLDELKYYI 298
 241 QSGRKADIMTGTGVCDCWKRTIFRDEGKAFKFGKMSVNLKMGAFVLVYLDELKYYI 298

```

Db      1 MTDAAISFAKDFLAGGVAASIKTAVAPIERVKLLVOYHASKQITADKQKGMDCVVR 60
QY      61 IPKEGVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 IPKEGGLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLQNVDRKTFWRFRFAGNLASG 120
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGDCLVYTKKSDGINKLYOGFSVS 180
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 GAAGATSLCFYVPLDFARTRLAADVGKADREFGLDCLAKIFRSDGLKGLYOGFNV 180
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      181 VOGIIYRAAYRGVYDTAKGMLDPKKNHIYVSMIAQVTVAVAGVSYPTVRRRMM 240
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 VOGIIYRAAYRGVYDTAKGMLDPKKNHIYVSMIAQVTVAVAGVSYPTVRRRMM 240
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      241 QSGRKADIMYTGVDCKWKIRFRDEGKAFKFGANSNLRGKGAFLVLYDELKVI 298
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 QSGRKGAELMYSGITDCKWKIARDBGSRAFFRGANSNLRGKGAFLVLYDELKVI 298
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 10

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Q95YX4 PRELIMINARY; PRT: 299 AA.
ID      095YX4
AC      095YX4:
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      ADP-ATP translocator.
OS      Ethmostigmus rubripes.
OC      Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
OC      Pleurostomatophora; Scolopendromorpha; Scolopendridae; Ethmostigmus.
OX      NCBI_TaxID=62613;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Burrell J.N.;
RT      "Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus
RT      rubripes."
RL      Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF401758; AAL02100.1;
DR      InterPro; IPR001993; Mitoch_carrier.
DR      InterPro; IPR002067; Mlt_carrier.
DR      Pfam; PF00153; mltc_carr; 3.
DR      PRINTS; PR00926; MITOCH_CARRIER.
DR      PROSITE; PS00215; MITOCH_CARRIER; 3.
SQ      SEQUENCE 299 AA; 33037 MW; 3C3BCB26E7C3C5E CRC64;

```

Query Match 84.3%; Score 1300; DB 5; Length 299;
 Best Local Similarity 81.5%; Pred. No. 1.5e-109;
 Matches 243; Conservative 26; Mismatches 29; Indels 0; Gaps 0;

```

QY      1 MTEQAISFAKDFLAGGIAAISKTAVAPIERVKLLVOYHASKQITADKQKGMDCVVR 60
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MPIDAVSLKDFIAGGVAASIKTAVAPIERVKLLVOYHASKQITADKQKGMDCVVR 60
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61 IPKEGVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 IPKEGGLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLQNVDRKTFWRFRFAGNLASG 120
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGDCLVYTKKSDGINKLYOGFSVS 180
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGDCLVYTKKSDGINKLYOGFSVS 180
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      181 VOGIIYRAAYRGVYDTAKGMLDPKKNHIYVSMIAQVTVAVAGVSYPTVRRRMM 240
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 VOGIIYRAAYRGVYDTAKGMLDPKKNHIYVSMIAQVTVAVAGVSYPTVRRRMM 240
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      241 QSGRKADIMYTGVDCKWKIRFRDEGKAFKFGANSNLRGKGAFLVLYDELKVI 298
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 QSGRKADILYKNTIDCKWKIKYKTEGGAFFKGAFLVLYDELKVI 298
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 11

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Q91336 PRELIMINARY; PRT: 317 AA.
ID      Q91336

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AC      Q91336;
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      ADP-ATP translocase.
OS      Rana sylvatica (Wood frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX      NCBI_TaxID=45438;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Tissue=Liver;
RC      MEDLINE=97398141; PubMed=9256066;
RX      Cai O., Storey K.B.;
RT      "Differential regulation of the mitochondrial ADP/ATP translocase gene
RT      in wood frogs under freezing stress."
RL      Biochim. Biophys. Acta 1353:69-78(1997).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Tissue=Liver;
RC      Tissue=Liver;
RX      Cai O., Storey K.B.;
RL      Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
CC      -1. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR      EMBL; U44832; AA97882.2;
DR      InterPro; IPR001993; Mitoch_carrier.
DR      InterPro; IPR002067; Mlt_carrier.
DR      Pfam; PF00153; mltc_carr; 3.
DR      PRINTS; PR00926; MITOCH_CARRIER.
DR      PROSITE; PS00215; MITOCH_CARRIER; 3.
KW      Membrane; Transmembrane; Transport.
SQ      SEQUENCE 317 AA; 35005 MW; 5F66B7BD05CEB72 CRC64;

```

Query Match 81.6%; Score 1259; DB 13; Length 317;
 Best Local Similarity 86.8%; Pred. No. 8.2e-106;
 Matches 236; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

```

QY      1 MTEQAISFAKDFLAGGIAAISKTAVAPIERVKLLVOYHASKQITADKQKGMDCVVR 60
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MTDAAISFAKDFLAGGVAASIKTAVAPIERVKLLVOYHASKQITADKQKGMDCVVR 60
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61 IPKEGVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 IPKEGGLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLQNVDRKTFWRFRFAGNLASG 120
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGDCLVYTKKSDGINKLYOGFSVS 180
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGDCLVYTKKSDGINKLYOGFSVS 180
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      181 VOGIIYRAAYRGVYDTAKGMLDPKKNHIYVSMIAQVTVAVAGVSYPTVRRRMM 240
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 VOGIIYRAAYRGVYDTAKGMLDPKKNHIYVSMIAQVTVAVAGVSYPTVRRRMM 240
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      241 QSGRKADIMYTGVDCKWKIRFRDEGKAFKFGANSNLRGKGAFLVLYDELKVI 272
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 QSGRKGAELMYSGITDCKWKIARDBGSRAFFRGANSNLRGKGAFLVLYDELKVI 272
        ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 12

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Q81RA0 PRELIMINARY; PRT: 312 AA.
ID      Q81RA0;
AC      Q81RA0;
DT      01-MAR-2003 (TREMBLrel. 23, Created)
DT      01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      CG16944-PC.
GN      SESB.
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephydroidea; Drosophilidae; Drosophila.
OX      NCBI_TaxID=7227;
RN      [1]
RP      SEQUENCE FROM N.A.

```


RA MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananthides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.C., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Branton R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfankoch C., Baldwin D.,
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostel C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Lammel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasok P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshneft A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Ralner K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spletter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector A.C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissensbach J.,
 RA Williams S.M., Woodgett, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster";
 RA Science 287:2185-2195(2000).
 [12]
 RA SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Krommler B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Ananthides P.G., Branton R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Idegawa C., Jalali M., Kruse D., Li P., Mattei B., Moshneft A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacle J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Pionneuvong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RA "sequencing of Drosophila melanogaster genome";
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [13]
 RA SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 RA Ciamp M., Dysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommler B., Marshall B., Milburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutnak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RA "Annotation of Drosophila melanogaster genome";
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [14]
 RA SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [15]
 RA SEQUENCE FROM N.A.

RA flyBase;
 RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RA EMBL: AE003484; AAN09267.1;
 RA SEQUENCE 312 AA; 34214 MW; 78D5634E74E1680F CRC64;
 SO
 Query Match 81.3%; Score 1254.5; DB 5; Length 312;
 Best Local Similarity 80.6%; Pred. No. 2.1e-105;
 Matches 237; Conservative 23; Mismatches 33; Indels 1; Gaps 1;
 5 AISPADFAGGAAIAISKTAIVAPIERVKLLLOVQHASKQIADKQKGIIVDQIVRPKE 64
 20 AAGVAVDFAGGISAASKTAIVAPIERVKLLLOVQHSKQISPDQKQGVDFIRPKKE 79
 65 OGVLSEFRGNLANVIRFFPTQALNFAFKDKYKQIFLGVDVKTQFWRFFAGNLASGGAAG 124
 80 OGFSFWRGNLANVIRFFPTQALNFAFKDKYKQIFLGVDVKTQFWRFFAGNLASGGAAG 139
 125 ATSLCFYPLDFAFTRIAADVGSKGEREREGCLDCLVKTGSDGIRGLYOGFSVVOGI 164
 140 ATSLCFYPLDFAFTRIAADVKGKQ-OREFTGLGNCITLTKFKSDGIVGLYRGCGVVOGI 198
 185 IIRAAVFGYDPAKGLPDKNTHYVSMINQTVAVGVSYSPDTRRRMMOSGR 244
 199 IIRAAVFGYDPAKGLPDKNTPIYSAIAQVTVVAGIVSYSPDTRRRMMOSGR 258
 245 KGADIMYTGTVDCWKIFRDEGKAFKFGKAMSVLRGCGAFVLYVDELKVI 298
 259 KAEVYIKNTLHCWATIAKQEGAFKAFNSILRGTGAFVLYVDELKVI 312
 DB
 RESULT 13
 ID Q9NHM5 PRELIMINARY; PRT; 300 AA.
 AC Q9NHM5
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Lucilia.
 OX NCBI_TaxID=7375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SS mal seeking;
 RT "A cDNA clone encoding the ADP/ATP translocase of Lucilia cuprina";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF218587; AAF32322.1; -
 DR Interpro: IPR001993; Mitochondrion carrier.
 DR Interpro: IPR002067; Mitochondrion carrier.
 DR Pfam: PF00153; mltc_carr; 3.
 DR PRINTS: PR00926; MITOCH_CARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER.
 KM Membrane; Transmembrane; Transport.
 SO SEQUENCE 300 AA; 33036 MW; 5459DF0EA0E2E742 CRC64;
 Query Match 80.1%; Score 1235.5; DB 5; Length 300;
 Best Local Similarity 79.5%; Pred. No. 1e-103;
 Matches 233; Conservative 24; Mismatches 35; Indels 1; Gaps 1;
 6 ISPAKDFLAGGIAAISKTAIVAPIERVKLLLOVQHASKQIADKQKGIIVDQIVRPKE 65
 9 LGFVKDFPAGGISAASKTAIVAPIERVKLLLOVQHSKQISPDQKQGMIDCYVRIPKEQ 68
 66 GVLSEFRGNLANVIRFFPTQALNFAFKDKYKQIFLGVDVKTQFWRFFAGNLASGGAAGA 125
 69 GVLSEFRGNLANVIRFFPTQALNFAFKDKYKQIFLGVDVKTQFWRFFAGNLASGGAAGA 128
 126 TSLCFYPLDFAFTRIAADVGSKGEREREGCLDCLVKTGSDGIRGLYOGFSVVOGI 165

DB 129 TSLCFVYPLDPFARTRLAADTKG-QREFTLGNCIAKIFKSDGLVGLRGFVSVGCI 187
 QY 186 IYRAAYGVYDTAKGMLPDPKNTIIVSWMIQVTVAVAGVSPEDTVRRMMQSGRK 245
 DB 188 IYRAAYGVYDTAKGMLPDPKNTIIVSWMIQVTVAVAGVSPEDTVRRMMQSGRK 247
 QY 246 GADIMYGTVDCKMKRIFRDEGKAFKFGANSVLRGMGAVLVLYDELKAVI 298
 DB 248 ATEIITKNTLHCWMTIAKOE-GTAFKGFAGFNSVLRGTGGAFLVLYDEIKKFL 300

RESULT 14

044093 PRELIMINARY; PRT; 288 AA.
 ID 044093;
 AC 044094;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE ADP/ATP translocase (Fragment).
 GN SESB.
 OS Drosophila pseudoobscura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7237;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
 RL Genetics 0:0-0(1997).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AF025799; AAB87883.1; -.
 DR Flybase; FBgn0023292; Dpse\sesb.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR Membrane; Repeat; Transmembrane; Transport.
 FT NON_TER 288
 SQ SEQUENCE 288 AA; 31725 MW; 052B0CC0050436B0 CRC64;

Query Match 77.0%; Score 1187.5; DB 5; Length 288;
 Best Local Similarity 80.7%; Pred. No. 2.2e-99;
 Matches 230; Conservative 19; Mismatches 33; Indels 3; Gaps 3;

QY 5 AISEFAKDLGAGIAAISKTAAPIERVKLLQVOHASKQIADQYKGIYDCIYRIKE 64
 DB 7 AMGFVKDPAAGISAAVSKTAAPIERVKLLQVOHISKQISPDQYGMVDCFTIRIKE 66
 QY 65 QGVLSFWRGNLANVIRYPTQALNFAFDKXKQIPLAGVDKHTQFWRFFAGNLASGAAG 124
 DB 67 QGFSEFWRGNLANVIRYPTQALNFAFDKXKQYVFLGVDKNTQFWRFFMGLASGAAG 126
 QY 125 ATSLCFVYPLDPFARTRLAADVGSCTEREFRGLDCLVYKISDGIKGLYOGFSVVOGI 184
 DB 127 ATSLCFVYPLDPFARTRLAADTKG-QREFTLGNCIAKIFKSDGLVGLRGFVSVVOGI 185
 QY 185 IYRAAYGVYDTAKGMLPDPKNTIIVSWMIQVTVAVAGVSPEDTVRRMMQSGR 244
 DB 186 IYRAAYGVYDTAKGMLPDPKNTIIVSWMIQVTVAVAGVSPEDTVRRMMQSGR 244
 QY 245 KGADIMYGTVDCKMKRIFRDEGKAFKFGANSVLRGMGAVLVLYDELKAVI 289
 DB 245 KATEIITKNTLHCWMTIAKOE-GTAFKGFAGFNSVLRGTGGAFLVLY 288

RESULT 15

044094 PRELIMINARY; PRT; 288 AA.
 ID 044094;
 AC 044094;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE ADP/ATP translocase (Fragment).
 GN SESB.
 OS Drosophila subobscura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7241;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
 RL Genetics 0:0-0(1997).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AF025799; AAB87884.1; -.
 DR Flybase; FBgn0023237; Dsub\sesb.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR Membrane; Repeat; Transmembrane; Transport.
 FT NON_TER 288
 SQ SEQUENCE 288 AA; 31775 MW; 06A1D1E477E81B26 CRC64;

Query Match 76.7%; Score 1183.5; DB 5; Length 288;
 Best Local Similarity 80.4%; Pred. No. 5e-99;
 Matches 229; Conservative 20; Mismatches 33; Indels 3; Gaps 3;

QY 5 AISEFAKDLGAGIAAISKTAAPIERVKLLQVOHASKQIADQYKGIYDCIYRIKE 64
 DB 7 AMGFVKDPAAGISAAVSKTAAPIERVKLLQVOHISKQISPDQYGMVDCFTIRIKE 66
 QY 65 QGVLSFWRGNLANVIRYPTQALNFAFDKXKQIPLAGVDKHTQFWRFFAGNLASGAAG 124
 DB 67 QGFSEFWRGNLANVIRYPTQALNFAFDKXKQYVFLGVDKNTQFWRFFMGLASGAAG 126
 QY 125 ATSLCFVYPLDPFARTRLAADVGSCTEREFRGLDCLVYKISDGIKGLYOGFSVVOGI 184
 DB 127 ATSLCFVYPLDPFARTRLAADTKG-QREFTLGNCIAKIFKSDGLVGLRGFVSVVOGI 185
 QY 185 IYRAAYGVYDTAKGMLPDPKNTIIVSWMIQVTVAVAGVSPEDTVRRMMQSGR 244
 DB 186 IYRAAYGVYDTAKGMLPDPKNTIIVSWMIQVTVAVAGVSPEDTVRRMMQSGR 244
 QY 245 KGADIMYGTVDCKMKRIFRDEGKAFKFGANSVLRGMGAVLVLYDELKAVI 289
 DB 245 KATEIITKNTLHCWMTIAKOE-GTAFKGFAGFNSVLRGTGGAFLVLY 288

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 Job time : 51.3897 secs

